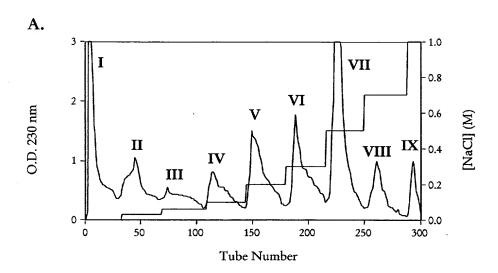


Fig. 1.0





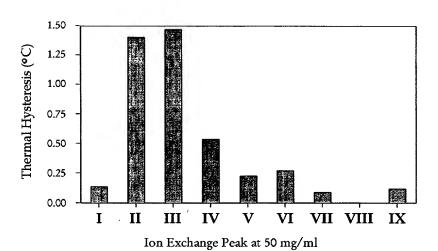


Fig. 1.1

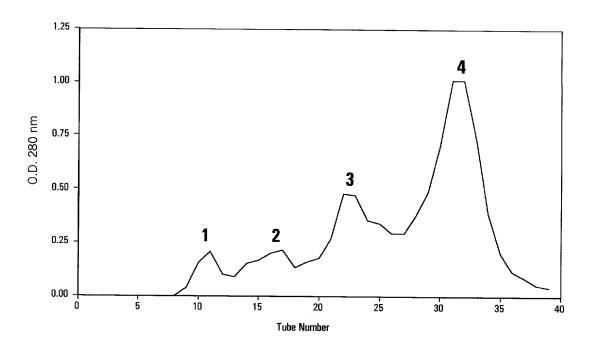
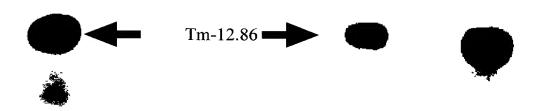
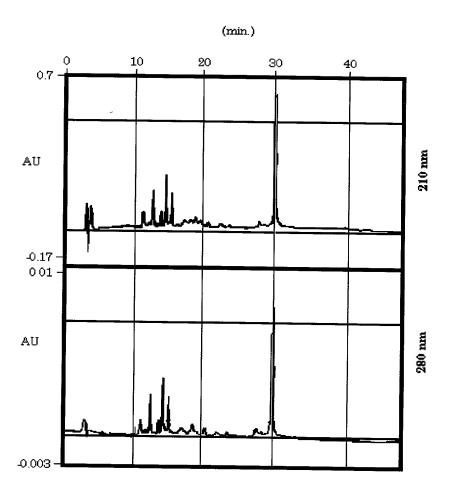


Fig. 1.2



12.5 25

Fig. 1.3 Fig. 1.4



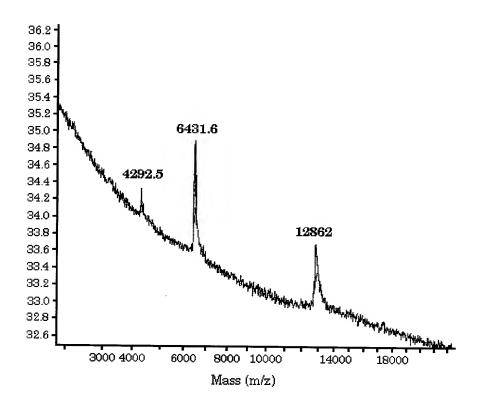
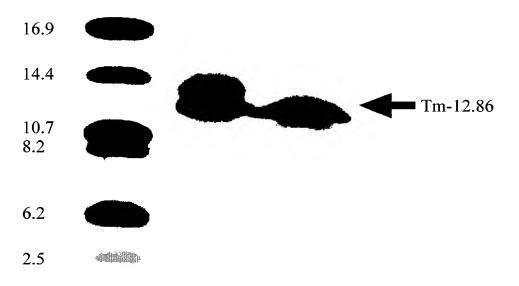
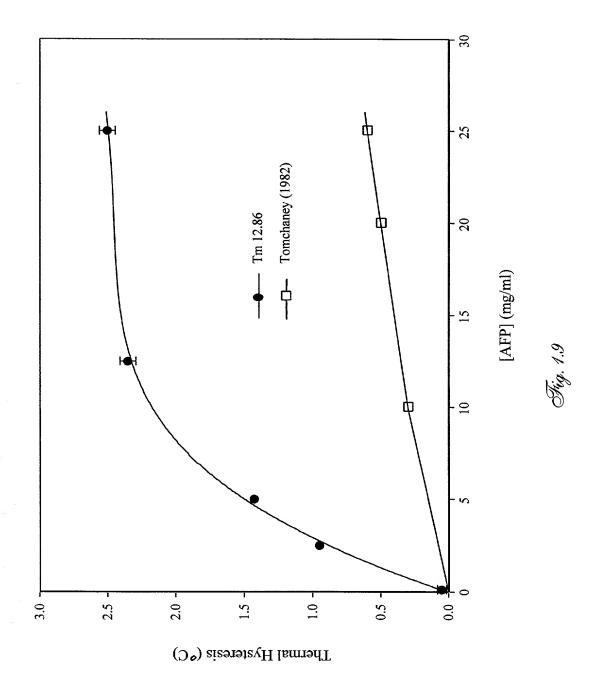


Fig. 1.6



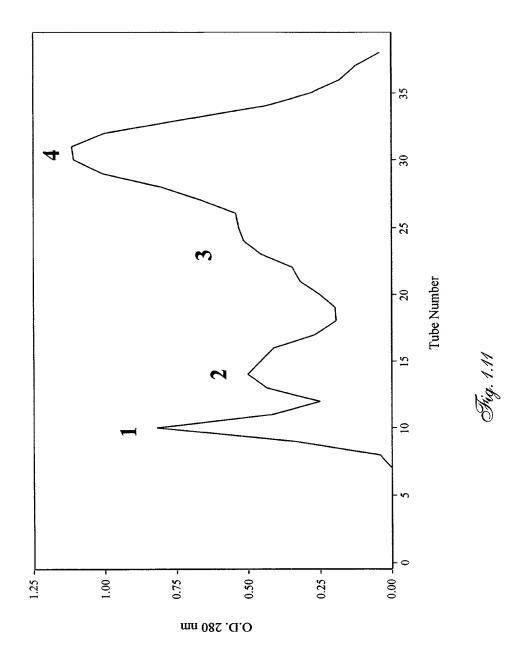
w w/o

Fig. 1.7



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32.3
17.4
7.5

Fig. 1.10



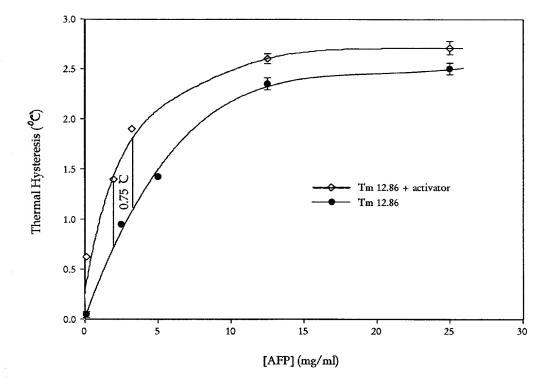


Fig. 1.12

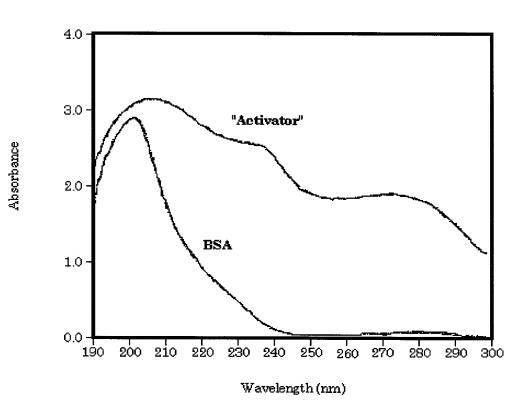


Fig. 1.13

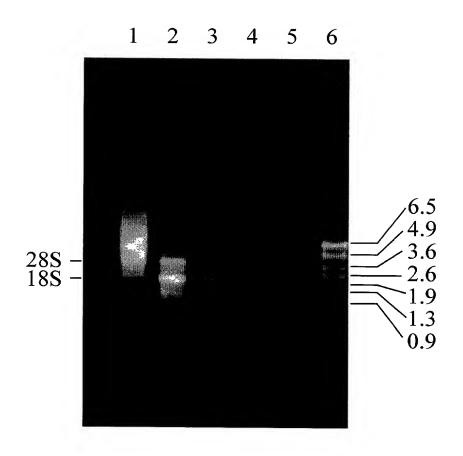
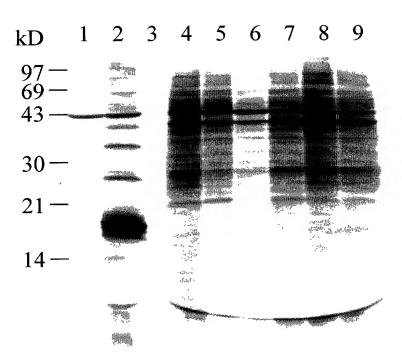


Fig. 2.0



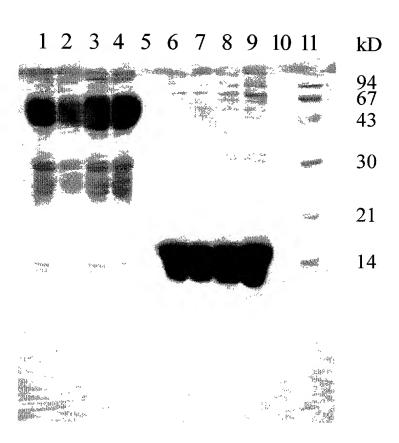


Fig. 2.2

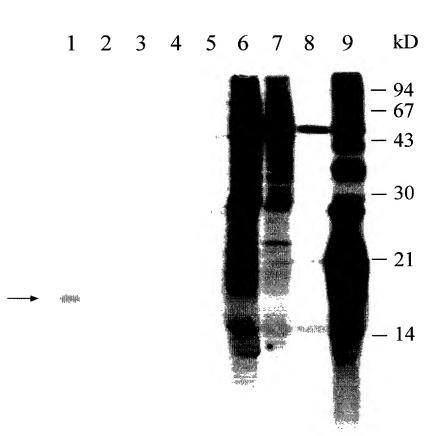
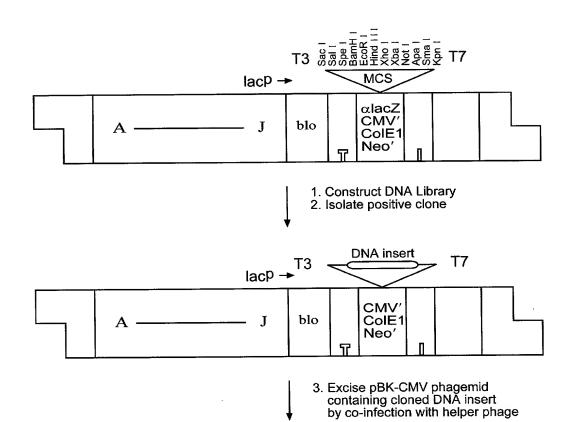


Fig. 2.3



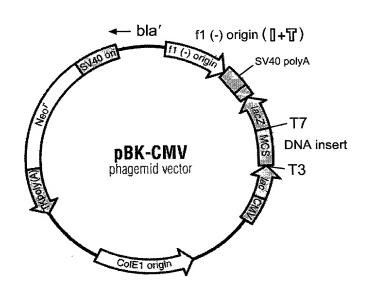
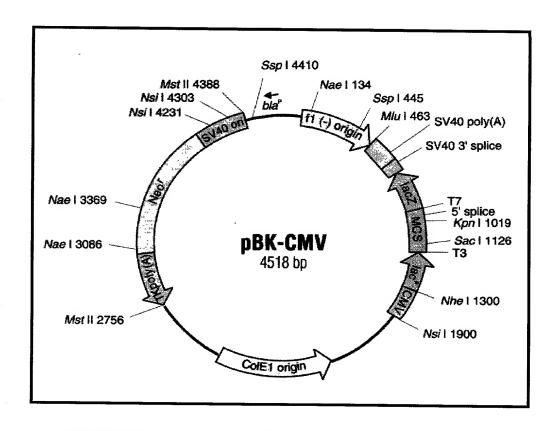
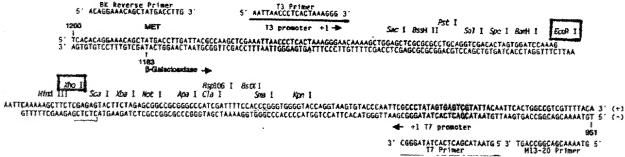


Fig. 2.4a





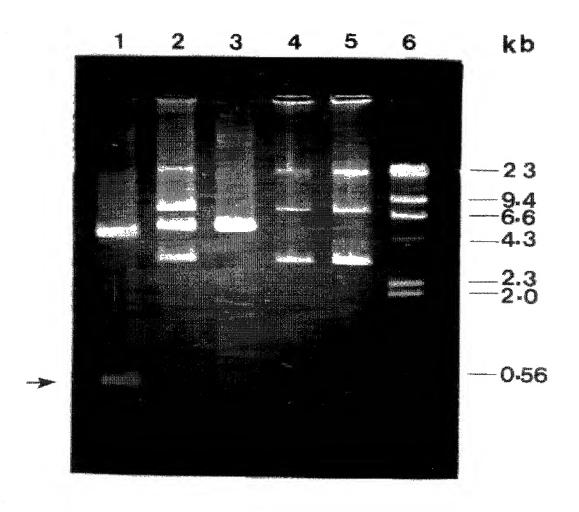


Fig. 2.5

DNA sequence of Tm 13.17 cDNA clone

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537 AGAGTATTCTAGAGCGGCCGGGCCCATCGTTTCCACCC

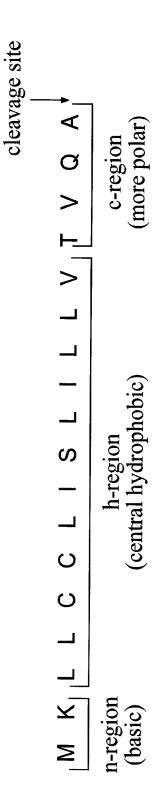


Fig. 2.66

A. Mature Tm 13.17 amino acid residure

- 1 LTEAQIEKLN KISKKCQNES GVSQEIITKA RNGDWEDDPK LKRQVFCVAR
- 51 NAGLATESGE VVVDVLREKV RKVTDNDEET EKIINKCAVK RDTVEETVFN
- 101 TFKCVMKNKP KFSPVD

B. Summary of the composition analysis for the mature Tm 13.17 sequence:

Resid	due	Number	Mole Percent
A = B = C =	Asx	6 0 4	5.172 0.000 3.448
E =		8 13	6.897 11.207
F = G = H =	Gly	4 4 0	3.448 3.448 0.000
I = K = I	Ile	6 16	5.172 13.793
L = М = N =	Met	5 1 8	4.310 0.862
P = Q =	Pro	3 4	6.897 2.586 3.448
R = S =	Ser	6 5	5.172 4.310
T = V = V = V = V = V = V	/al	8 14 . 1	6.897 12.069 0.862
	Tyr	0 0	0.000

Molecular weight = 13171.96; Residues = 116; Average Residue Weight = 113.551

Charge = 1; Isoelectric point = 7.74.

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                   81
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AFP-3	1	ETPREKLKQHSDACKAESGVSEESLNKVRNREEVDDPKLKEHAFCILKRA 5	0
Tm 13.17	53	GLATESGEVVVDVLREKVRKVTDNDEETEKIINKCAVKRDTVEETVFNTF 1 :	.02
AFP-3	51	GFIDASGEFQLDHIKTKFKENSEHPEKVDDLVAKCAVKKDTPQHSSADFF 1	.00
Tm 13.17	103	KCVMKNKP 110	
AFP-3	101	KCVHDNRS 108	

Percent identity: 39.8 (identical amino acids; Percent similarity: 58.3 (identical amino acids plus conservative amino acids).

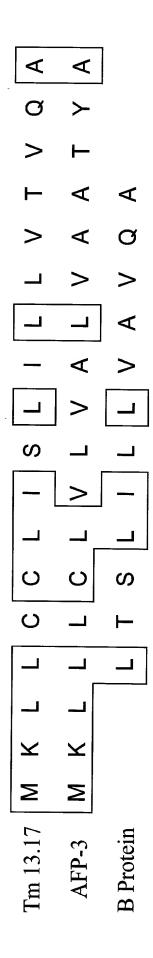
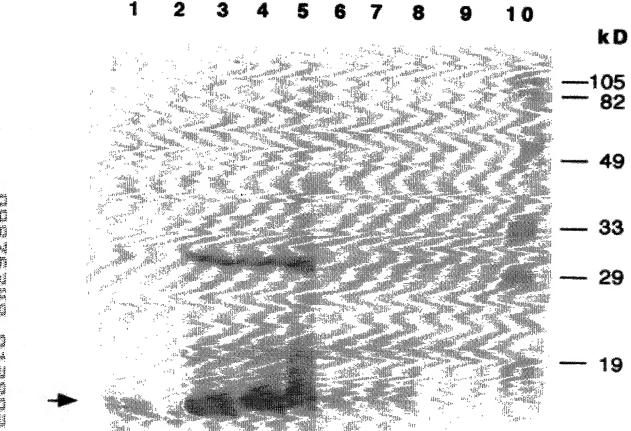
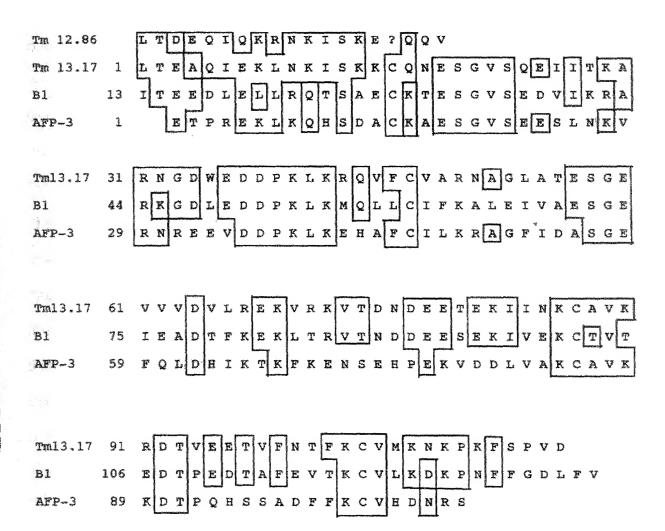


Fig. 2.9

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Fig 2.10





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1	GGC) A	С	G.	A (3 C	; A	A	A	_	A T	r G]A K			C 1		C		C	-	G	T		C T			G (CO		С	
47	ATC	G V		C.	A 7	r c	G						A	G	G	-			С		cc	G	Ā	С		A		A		ιT					
92	A G G	A £ N	• •		A A K	A G	i A I	τ		A (G C	S A K			G E		T C			C.		à C Q			G T V	G	TS		0			G 7 V	G	T S	СС
137	C A A	G E			A C	C G	A I	T		G / D	A (C A K			G V	TC	C			A T	C A	G			G 1 V	c	T L	Τ (G (С	G A D	C	G D	ΑТ
182	CCC	C A K			A 1 M			A				3 C H				TC						F			T (S		A		G A			A C	T	G G	G A
226	GT C	G A	_		A (c c	G			G (A	CC		i G			A C				A N			T				G V) Т -	С	A A K	\ A	G A	СС
271	A A G	G C L	-		A A		G C		-	G ⁻ V		G A	-		A S						A A				G 1 V	G	G D		C A K			A 7 I	c	G V	TG
316	CAG	3 A K			T (3 C	G V									A C		C			C A					\ G	G		A <i>A</i>		G	G C A	T	T Y	ΑТ
361	G A C	A C	С	C	T T	ГС	A K		G	T (G 7	ΓA	•	•	-	A C	_	i A	_	A S	G T				C C	т	G D	Α.	T 7	T T	С	T C S	T	CP	СТ
406	ATT	r G D		Т	Τ,	A <i>A</i>	T	Т	G	Τ.	T	T	G	Т	A	т 1	т	G	Α	С	TO	àΑ	A	Т	TI	Т			-			A A		•	
451	ACT	ГΑ	Т	С	G-	ΤT	- A	Т	G	A	A A	AΑ	A	A	Α	A A	۱.A	A	Α	Α	A A	۱A	Α	Α			*				•				

poly (A) tail

Start

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G G C A C G A G C A A A A T G A A A C T C C T C T T G T G C T T T G C G
2-2
     G G C A C G A G C A A A A T G A A A C T C C T C T T G C T T T G C T T
2-3
     T T C G C C G C C A T C G T C A T C G G A G C T C A G G C T C T C A C C G
2-2
2-3
      T T C G C C G C C A T C G T C A T C G G A G C T C A G G C T C T C A C C G
2-2
     A C G A A C A G A T A C A G A A A A G G A A C A A G A T C A G C A A A G A
     A C G A A C A G A T A C A G A A A A G G A A C A A G A T C A G C A A A G A
2-3
     A T G C C A G C A G G T G T C C G G A G T G T C C C A A G A G A C G A T C
2-2
    . A T G C C A G C A G G T G T C C G G A G T G T C C C A A G A G A C G A T C
2-2
     G A C A A A G T C C G C A C A G G T G T C T T G G T C G A T G A T C C C A
2-3
     GACAAAGT CCGCACAGGTGTCTTGGTCGAlclGATCCCA
     A A A T G A A G A A G C A C G T C C T C T C C T C T C G A A G A A A C
2-2
2-3
     A A A T G A A G A A G C A C G T C C T C T C T C T C G A A G A A A C
2-2
     2-2
     G T A C T C A A A G C C A A G C T G A A G C A T G T G G C C A G C G A C G
2-3
     G T A C T C A A A G C C A A G C T G A A G C A T G T G G C C A G C G A C G
     A A G A G G T G G A C A A G A T C G T G C A G A G T G C G T G G T C A A
2-2
     A A G A A G T G G A C À A G A T C G T G C A G A A G T G C G T G G T C A A
2-3
2-2
     G A A G G C C A C A C C A G A G G A A A C G G C T T A T G A C A C C T T C
     G A A G G C C A C A C C A G A G G A A A C G G C T T A T G A C A C C T T C
2-3
     A A G T G T A T T T A C G A C A G C A A A C C T G A T T T C T C T C C T A
2-2
     A A G T G T A T T T A C G A C A G T A A A C C T G A T T T C T C T C C T A
2-3
2-2
     T T G A T T A A T T GTTTTGTATTTGACTGAATTTTGACAA
     T T G A T T A A T T GTTTTGTATTTGACTGAATTTTGACAA
2-3
     T A A A G G T A AT A T C G T T A T G T A A A A
2-2
     T A A A G G T A C T A T C G T T A T G A A A A A
2-3
```

Predicted Amino Acid

Composition of 2-2 and 2-3

Analysis	Whole Protein
Molecular Weight	12843.80 m.w.
Length	115
1 microgram =	77.859 pMoles
Molar Extinction coefficient	3040±5%
1 A(280) =	4.22 mg/ml
Isoelectric Point	7.11
Charge at pH 7	0.13

Whole Protein Composition Analysis	Whole	Protein	Composition	Analysis
------------------------------------	-------	----------------	-------------	----------

	Number	% by	% by
Amino Acid(s)	count	weight	frequency
Charged (RKHYCDE)	48	47.19	41.74
Acidic (DE)	20	18.90	17.39
Basic (KR)	20	20.40	17.39
Polar (NCQSTY)	30	25.35	26.09
Hydrophobic (AILFWV)	34	27.26	29.57
A Ala	6	3.32	5.22
C Cys	4	3.21	3.48
D Asp	11	9.86	9.57
E Glu	9	9.05	7.83
F Phe	3	3.44	2.61
G Gly	4	1.78	3.48
H His	2	2.14	1.74
l lle	6	5.29	5.22
. K Lys	18	17.97	15.65
L Leu	5	4.41	4.35
M Met	1	1.02	0.87
N Asn	· 2	1.78	1.74
P Pro	4	3.02	3.48
Q Gln	6	5.98	5.22
R Arg	2	2.43	1.74
S Ser	7	4.75	6.09
T Thr	9	7.08	7.83
V Val	14	10.80	12.17
W Trp	0	0.00	0.00
Y Tyr	2	2.54	1.74
B Asx	0	0.00	0.00
Z Glx	0	0.00	0.00
X Xxx	0	0.00	0.00
. Ter	0	0.00	0.00

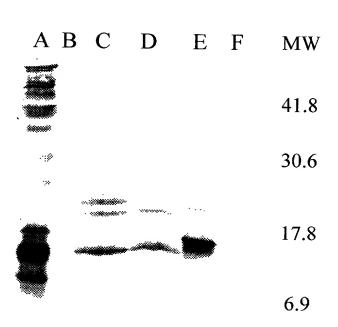
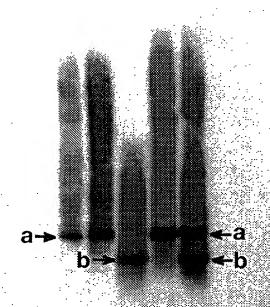


Fig. 3.4



1 2 3 4 5



577 bp

483 bp

Fig. 4.0

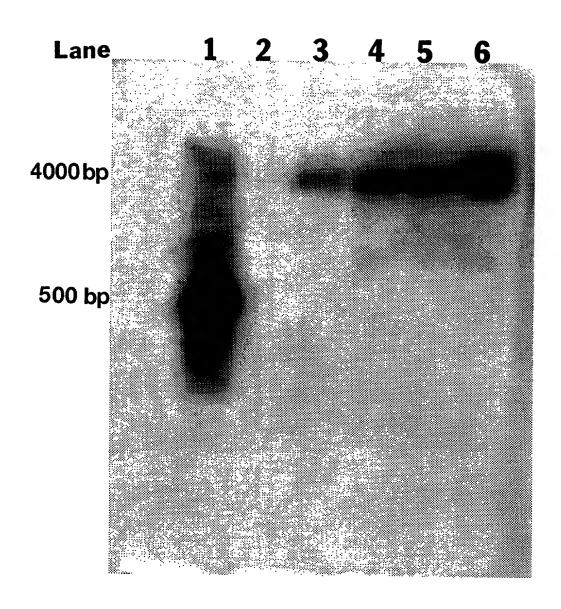
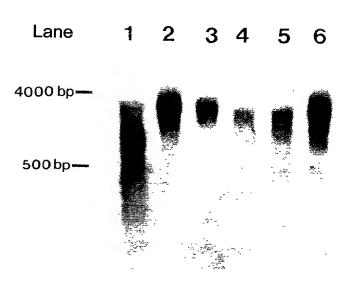
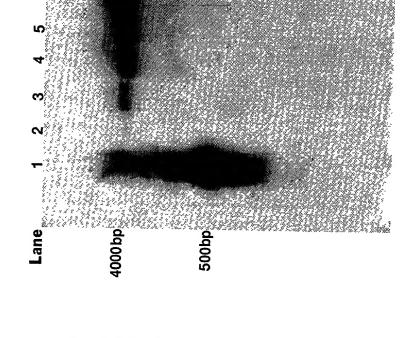


Fig. 4.1



Lane

4000b



Lane 1 2 3 4 5 6



Lane 1 2 3 4 5

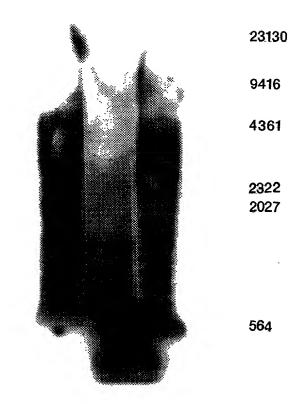


Fig. 4.5

Tm 13.17 cDNA

Ŧ	MOTO	1.223.1	CA	AAC	AAJ	rrce		CG	CAC	.TAC	'I'AA	GAT	GAL	GTT	GCI	CTG	TTC	TCI	'AA'	'CT
												M	K	L	L	C	C	<u>L</u>	I	<u>_</u> S
61	CCCT	CAT	TCT	'GT'I	GGT	CAC	'AGI	TCA	\GG(CCI	GAC	CGA	GGC	ACA	AAT	TGA	GAA	ACT	GAA	.CA
	<u>L</u>		<u>L</u>	<u>L</u>	V	T	V	Q	<u>A</u>	Å L	T Forw	E ard F	A Prime	Q	I	E	K	L	N	K
121	AGAT	CAG	CAA	AAA	ATG	TCA	AAA	TGA	AAC						GAT	CAT	AAC	CAA	AGC	TC.
	I	S	K	K	C	Q	N	E	S	G	V	S	Q	E	I	I	T	K	A	R
181	GCAA	CGG	TGA	CTG	GGA	GGA	CGA	TCC	TAA	ACT	'GAA	ACG	CCA	AGT	TTT	TTG	CGI	'GGC	CAG	GA
	N	G	D	W	E	D	D	P	K	Ļ	K	R	Q	V	F	C	V	A	R	N
241	ACGC	CGG	TCT	GGC	CAC	:GGA	ATC	:GGG	AGA	GGI	GGT	GGT	CGA	CGT	GTT	GAG	GGA	GAA	GG1	'GA
	A	G	L	A	T	E	S	G	E	V	V	V	D	v	L	R	E	K	V	R
301	GGAA	GGT	CAC	TGA	.CAA	CGA	CGA	AGA	AAC	TGA	GAA	TAA	CAT	CAA	TAA	GTG	CGC	CGT	CAA	GA
	K Rev	v erse	T Prin	D ner	N	. D	E	E	T	E	K	I	I	N	K	C	A	٧	K	R
361	GAGA	TAC	TGT	TGA	AGA	GAC	GGT	GTI	CAA	TAC	TTT	CAA	ATG	TGT	CAT	GAA	AAA	CAA	GCC	AA
	D	T	V	E	E	T	V	F	N	T	F	K	С	V	M	K	N	K	P	K

421 AGTTCTCACCAGTTGATTGAACCACCACGACTAGTAGATGGTTCAAATGGTGTGCTTTAC

F S P V D *

Forward Primer

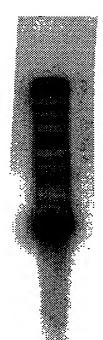
2-2	LTDEQIQKRNKI SKECQQVS <mark>GVSQE</mark> TI DKVRTGVLV
Tm 13.17	LTEAQIEKLNKI SKKCQNESGVSQEI I TKARNGDWE
B2	LTEEDLQLLRQTSAECKTES GASEA VI KKARKGDLE
AFP-3	ETPREKLKQHSDACKAES <mark>GVSEE</mark> SLNKVRNREEV
2-2 Tm 13.17 B2 AFP-3	D D P K M K K H V L C F S K K T G V A T E A G D T N V E V L K A K L K H D D P K L K R Q V F C V A R N A G L A T E S G E V V V D V L R E K V R K D D P K L K M Q L L C I F K A L E I V A E S G E I E A D T F K E K L T R D D P K L K E H A F C I L K R A G F I D A S G E F Q L D H I K T K F K E
2-2 Tm 13.17 B2 AFP-3	Reverse Primer VAS DEEVDKI VQKCVVKKATPEET AYDTFKCIYDS VTDNDEETEKII NKCAVKRDTVEETVFNTFKCVMKN VTNDDEESEKI VEKCTVTEDTPEDTAFEVTKCVLKD NSEHPEKVDDL VAKCAVKKDTPQHSSADFFKCVHDN
2-2	KPDFSPID
Tm 13.17	KPKFSPVD
B2	KPNFFGDLFV
AFP-3	RS

Fig. 4.6b

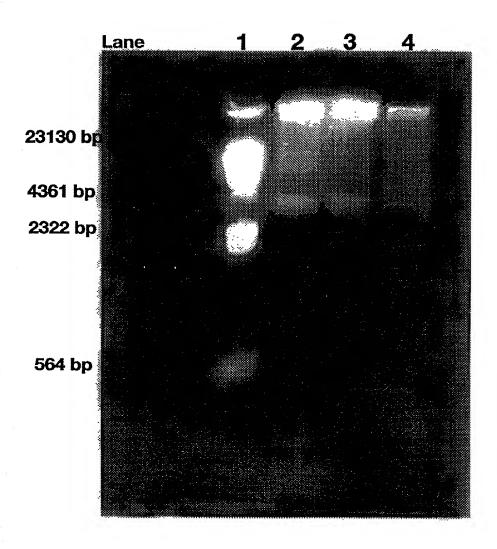
percent % composition

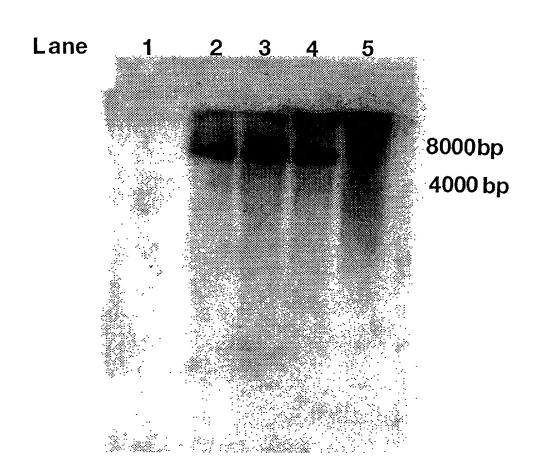
Primer	A	С	G	Т	MeltingTemperature(°C)	
Forward	28.6	14.3	42.9	14.3	44.0	
Reverse	25.0	31.3	6.3	37.5	44.0	

Fig. 4.6c



3600 bp





1	GGCACG	SAGCAAAA	ATGAAACTCCT M K L L	CTTGTGCTTT L C F	GCTTTCGCCGCC A F A A
47	ATCGTC	ATCGGAC	CTCAGGCTCTC	CACCGACGAAC T D E Q	AGATACAGAAA I Q K
92	AGGAAC R N	CAAGATCA K I S	GCAAAGAATGC K E C	CAGCAGGTGT Q Q V S	CCGGAGTGTCC G V S
137	CAAGAG Q E	GACGATCO T I E	ACAAAGTCCGC K V R	ACAGGTGTCT T G V L	T G G T C G A C G A T V D D
182	CCCAAA P K	ATGAAGA M K K	AGCACGTCCTC H V L	TGCTTCTCGA C F S K	A G A A A C T G G A K T G
226	GTGGCA V A	ACCGAAC T E A	CCGGAGACACC G D T	AATGTGGAGG N V E V	TACTCAAAGCC L K A
271			AT GGCCAGCGAC	GAAGAGGTGG. E E V D	
316	CAGAAG Q K		TCAAGAAGGCC		
361	GACACC D T	TTCAAGO	ATTATTTACGAC	AGTAAACCTG S K P D	ATTTCTCTCCT F S P
406	ATTGAT	TAATTG1	TTTGTATTTGA	CTGAATTTTG	A C <u>A A T A A A</u> G G T
451	ACTATO	GTTATGI	· A A A A A A A A A		polyadenylation signal

poly (A) tail

Predicted Amino Acid

Composition of 3-4

Molecular Weight	12839.70 m.w.
Length	115
1 microgram =	77.883 pMoles
Molar Extinction coefficient	2920±5%
1 A(280) =	4.40 mg/ml
Isoelectric Point	7.14
Charge at pH 7	0.16

Whole Protein Composition Analysis

	Number	% by	% by
Amino Acid(s)	count	weight	frequency
Charged (RKHYCDE)	47	46.41	40.87
Acidic (DE)	20	18.91	17.39
Basic (KR)	20	20.41	17.39
Polar (NCQSTY)	29	24.55	25.22
Hydrophobic (AILFWV)	35	28.04	30.43
A Ala	6	3.32	5.22
C Cys	3	2.41	2.61
D Asp	11	9.86	9.57
E Glu	9	9.05	7.83
F Phe	3	3.44	2.61
G Gly	4	1.78	3.48
H His	2	2.14	1.74
1 lle	6	5.29	5.22
KLys	18	17.97	15.65
L Leu	5	4.41	4.35
M Met	1	1.02	0.87
N Asn	2	1.78	1.74
P Pro	4	3.02	3.48
Q Gin	6	5.99	5.22
R Arg	2	2.43	1.74
S Ser	7	4.75	6.09
T Thr	9	7.09	7.83
V Val	15	11.58	13.04
W Trp	0	0.00	0.00
Y Tyr	2	2.54	1.74
B Asx	0	0.00	0.00
Z Glx	0	0.00	0.00
X Xxx	0	0.00	0.00
. Ter	0	0.00	0.00

1	GG	C	Α	C	G /	A (3 C	A	A	Α		A M	Γ (G /	A A	A	C	T	С	C	Т	C ·	T 1 L	- (à T C		¢	T F	Т :	Γ (T	T F	Т	C	G (- C	G	с с -
47	A T	. с	G V	т	C /		гс	G			G A	c -		C A	4 0			T		Т		A T		0 0		Τ.		Α		C A	ı G	i A I	т		C.Q	Α (3 A K		Α
92	A G R	G	A	A (A A	A G	i A I	T		A S	G (A A		E			T C			C Q	A (G (G	G E	Α		T C	c	G		A	G V	T	3 T S	C	С
137,	C A	A	G	A (A (i A I	Т.			A (A <i>A</i>	\ \ \		С			С		C A			ìΤ	G V	Т		T T	· G	i G V		С	G D	A (0 0		Т
182	C C	С	A			A ⁻ M	re	i A K			A K			C A H	A (C					G			С	T S			A A	A G	à A R		A	A T	c -	r (Α
226	G T V	G	G A	C,	Α ;	A (c c	G	A	Α	G A	C	Ċ	G (3 <i>A</i>	A 6	à A)	C	A	С	С	A N	Α 7	۲ (ЭT /	G	G	Α	G	G T V	- Δ	C L	т	С	A K	Α,	A (a C	С
271	A A		L	T		A A	A G	à C H			G V			G (\		G		С				G A	A	G V			G A		A K			A I	т (C (G
316	C A	A G	κ			T (G C	Ç V			G V			A A				G					C /		g c	; A	G	Α		G / E	λ Α	A T		G	G A	c.	T 1		т
361	G A D	A C	A T	C		T '	T C	K			T V	G		A T	rī		T A	C	G			A S			A A	A	C			G A	A T	F		С	T S	c.	T C	çc	т
406	A T	Т	G	A	т :	T .	A A	T	Т	G	T	Т	Τ .	т (G T	Γ #	٦ ٢	т	Т	G	Α	С	Т (3 /	A A	·Τ	Т	T	T								_	a G ign	
451	Α (T	Α	T	С	G	TI	- Α	ιT	G	Α	Α	A.	A A	Α /	A <i>A</i>	A A	A	A	Α	Α	Α	A	۹,	4 Α	ι A				P	ر			-J ·					

poly (A) tail

Predicted Amino Acid

Composition of 3-9

Analysis	Whole Protein
Molecular Weight	12871.80 m.w.
Length	115
1 microgram =	77.689 pMoles
Molar Extinction coefficient	3040±5%
1 A(280) =	4.23 mg/ml
Isoelectric Point	7.11
Charge at pH 7	0.13

Whole Protein Composition Analysis

	Number	% by	% by
Amino Acid(s)	count	weight	frequency
Charged (RKHYCDE)	48	47.31	41.74
Acidic (DE)	20	18.86	17.39
Basic (KR)	20	20.57	17.39
Polar (NCQSTY)	30	25.29	26.09
Hydrophobic (AILFWV)	34	27.20	29.57
A Ala	6	3.31	5.22
C Cys	4	3.21	3.48
D Asp	11	9.84	9.57
E Glu	9	9.03	7.83
F Phe	3	3.43	2.61
G Gly	4	1.77	3.48
H His	2	2.13	1.74
1 lle	6	5.28	5.22
K Lys	17	16.93	14.78
L Leu	5	4.40	4.35
M Met	1	1.02	0.87
N Asn	2	1.77	1.74
P Pro	4	3.02	3.48
Q Gln	6	5.97	5.22
R Arg	3	3.64	2.61
S Ser	7	4.74	6.09
TThr	9	7.07	7.83
V Val	14	10.78	12.17
W Trp	0	0.00	0.00
Y Tyr	2	2.54	1.74
B Asx	0	0.00	0.00
Z Glx	0	0.00	0.00
X Xxx	0	0.00	0.00
. Ter	0_	0.00	0.00

1	G	3 C	Α	C	G A	A G	C	Α.	A A	\ A	A M	T		A A	A A	C	Т	C	C T	С	T	Т	G T			T T F	т	G A	С		_ T	С	G (c c	G A	СC
47	A 1	г с	G V	Τ (C A		С	G G	G A	A A	C	T	C A	A (à G A	i C	T	C.	ГC	A T	С	С	G A D	C	G	A A	Q			A -	ГΑ	CQ		3 A K		Α
92	A C	3 G	i A N	Α (C A			A T	т с	S			A A	A A	A G			T (G C	C			C A Q	G	G	TO	à T S			G (G A	G V		G T		С
137	C A	A A	G	Α¢	G A			A I	T (G	i A	С	A A	A A	۹ G V		С	C (G C	A			G G	ìΤ	G V	T (T L	Т		G ⁻ V	ГС	G		C G		T
182	C (P	С	A K			X T M		A K	A C	à A K			C A	A C	e V				τc				T T F	C	TS	C	A K			A A	4 A	A	-	Г G		A
226	G1 V	ΓG	G A	C /	A <i>A</i>			G.	A A	A G			G G	G A	G D			A (c c	A N			G T V	G	G	A C	G V			C -	ГС	A		A G		С
271	A A		i C L	Т	G A	\ A <	G	C H	Α 1	V	T	G		CC		G		G / D	A C	G	Α	Α	G A E		G V	TO	G D			A A		i A I	T	C G V		G
316	C/Q	A G	i A K	A (G T	T G	à C	G V	TC	a G V	T	С	A A	Α (à A K	A	G	G (c c	A T	С	Α	C C P	; A	G E	A C	G E			A (C G	G		ΓŢ		т
361	G A	A C	A T	C	C T F	T =	C	A K	A C	T E V	G	Т	A ·	TI	Υ	A	С	G / D	A C	A S	G	Т	A A K	A	C P	СТ	G D	Α	T	T - F	гс	T	c.	r c		Т
406	A T	ГΤ	G	Α.	ŢŢ	Γ.Α	A	Т	т (ЭT	Т	т	Т (G 1	Ā	·Τ	т	T	G G	i C	Т	G	A A	T	т	тт								_		
451	Α (СΤ	Α	т (c c	3 T	т	Α	TC	Ŧέ	Α	Α	Α.	A A	A A	·Α	Α	A	A A	A	Α	Α	ΑА	A			1	ĻΟ	ıya	æ	:11 y	ıäl	101	SI	gna	LE

poly (A) tail

Predicted Amino Acid

Composition of 7-5

Analysis	Whole Protein
Molecular Weight	12843.80 m.w.
Length	115
1 mlcrogram =	77.859 pMoles
Molar Extinction coefficient	3040±5%
1 A(280) =	4.22 mg/ml
Isoelectric Point	7.11
Charge at pH 7	0.13

Whole Protein Composition Analysis	Whole	Protein	Composition	Analysis
------------------------------------	-------	---------	-------------	----------

Whole Frotein Compositi	Number	% by	% by
Amino Acid(s)	count	weight	frequency
Charged (RKHYCDE)	48	47.19	41.74
Acidic (DE)	20	18.90	17.39
Basic (KR)	20	20.40	17.39
Polar (NCQSTY)	30	25.35	26.09
Hydrophobic (AILFWV)	34	27.26	29.57
A Ala	6	3.32	5.22
C Cys	4	3.21	3.48
D Asp	11	9.86	9.57
E Glu	9	9.05	7.83
F Phe	3	3.44	2.61
G Gly	4	1.78	3.48
H His	2	2.14	1.74
I IIe	6	5.29	5.22
KLys	18	17.97	15.65
L Leu	5	4.41	4.35
M Met	1	1.02	0.87
N Asn	2	1.78	1.74
P Pro	4	3.02	3.48
Q Gln	6	5.98	5.22
R Arg	2	2.43	1.74
S Ser	7	4.75	6.09
T Thr	9	7.08	7.83
V Val	14	10.80	12.17
W Trp	0	0.00	0.00
Y Tyr	2	2.54	1.74
B Asx	0	0.00	0.00
Z Glx	0	0.00	0.00
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Fig 4.13

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Fig. 4.14

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Tm 13.17	13.17	116	3.13	2.21	4.47	5.16	10.5	1.0	4.3	29.11	1.73	3.24 0		0	1.41 0 0	0		7.12	15.6	3.31	6.14	32.14
2-2	12.84	115	3.21	3.02	3.44	5.29	10.8	1.02 4.41	4.41	27.26	1.78	1.78 3.32 2.54 2.14	2.54	2.14	0	0	0	2.43	18.0	4.75	7.08	32.23
2-3	12.84	115	3.21	3.02	3.44	5.29	10.8	1.02 4.41	4.41	27.26	1.78	3.32	2.54	3.32 2.54 2.14	0	0	0	2.43 18.0		4.75	7.08	32.23
3-4	12.84	115	2.41	3.02	3.44	5.29	9.11	1.02	4.41	28.04	1.78	3.32	2.54	3.32 2.54 2.14	0	0	0	2.43 18.0		4.75	7.09	32.24
3-9	12.87	115	3.21	3.02	3.43	5.28	10.8	1.02	4.40	27.20	1.77		2.54	3.31 2.54 2.13 0	0	0	0	3.64 16.9		4.74	7.07	32.38
7-5	12.84	115 3.21	3.21	3.02	3.44	5.29	10.8	1.02	.02 4.41	27.26	1.78	1.78 3.32 2.54 2.14 0	2.54	2.14	0	0 0		2.43 18.0	18.0	4.75	7.08 32.23	32.23

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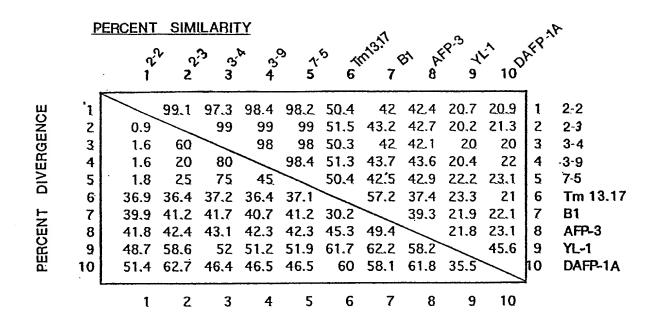
Fig. 4.16

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= conserved cysteine (yellow); Boxed = conserved residues in Genes (red)	LTEFDLE KLNKIS KKCONESGVSGETIDKV RAPPPRIGO CKTESGVSEDVIKRA RKGOOSPOWKNLSNNFGKAMOOCKTESGVSEDVIKRA RKGOOSPOWKNLCLNFGKAMOOCKTESGVSEDVIKRA RKGOODVOVTLGFKAMOOCKDELSLPOSVVADLYNFWYEGOVVOVWKOVTGKAFFWREOOVVOVTLGFKAFFWREOOVVOVTLGFKAFFWREOOVVOVTLGFKFFWREOOVVOVTLGFHFWREEFFHFWREOOVVOVTLGFKFFWREOOVVOVTLGFKFFWREOOVVOVTLGFKHFH OOVCKTESGLPVEVMOEFFHFWREOOVVOVTLGFHFWWFENOOVTEAAIKEFSOOGE	D D F K L K R D V F C V A R N A G L A T E S G E V V V D V L R E K L K H V A S D E E V D D D P K L K M Q L L C I F K A L E I V A E S G E I E A D T F K E K L T R V T N D D E E S E D D P K L K M Q L L C I F K A L E I V A E S G E I E A D T F K E K L T R V T N D D E E S E D D P K L K M Q L L C I F K A L E I V A E S G E I E A D T F K E K L T R V T N D D E E S E D D P K L K M Q L L C I F K A L E I V A D P D G N L H H G N A M E F A M K H G A D E T M A A D D L S N R D T G C A I I C C A I I C C A I I C C A I I C C A I I C C A S R H F N L L T D S S R M H H E N T D K F P N G A V L S F R M A K D L C M S N K F E L L D D D T R T H H V K M H D Y I K S F P N G D V L S E K M E E D E K C Y M N C L F H E F E V V D D N G D V H M E K L F A T V P L S M R D V L M E R L C C R A K C L R A C V M K K L D L D N D N G D V H L E K L F A T V P L S M R D V L N B E R E R K C L R A C V M K K L D L M D E S G K L N K E H A I E L V K V M S K H D A E K E D A E C D A E C C A I C C M S M K K L D L M D E S G K L N K E H A I E L V K V M S K H D A E K E D A E C D A E C C A I C C C A I C C C C C C C C C C C	V M K N K P K F K K K K K K K K K K K K K K K K
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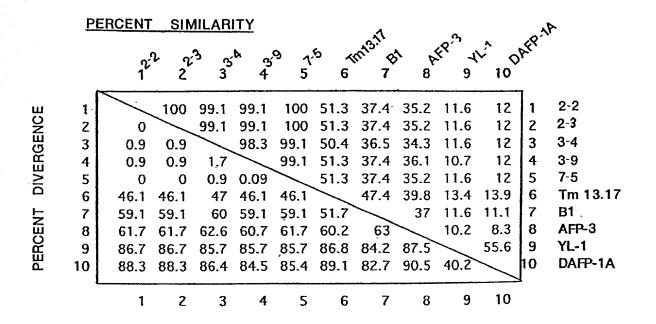
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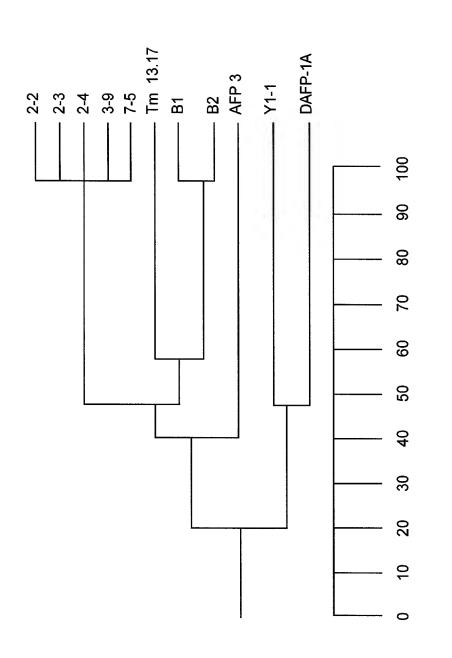
Fig. 4.18

### NUCLEOTIDE SEQUENCES



## AMINO ACID SEQUENCES





% Nucleic Acid Identity

Fig. 4.20

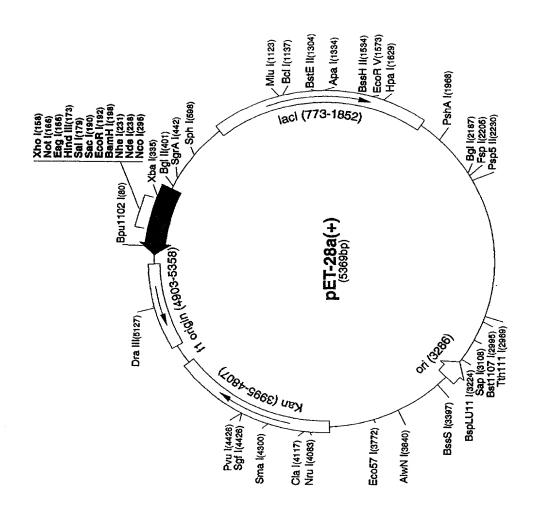
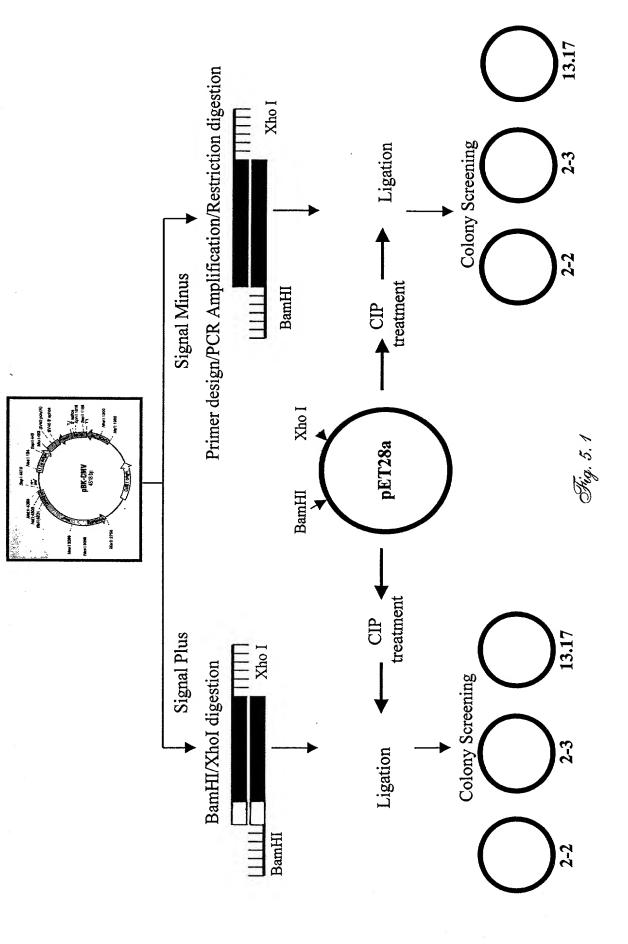


Fig. 5.0



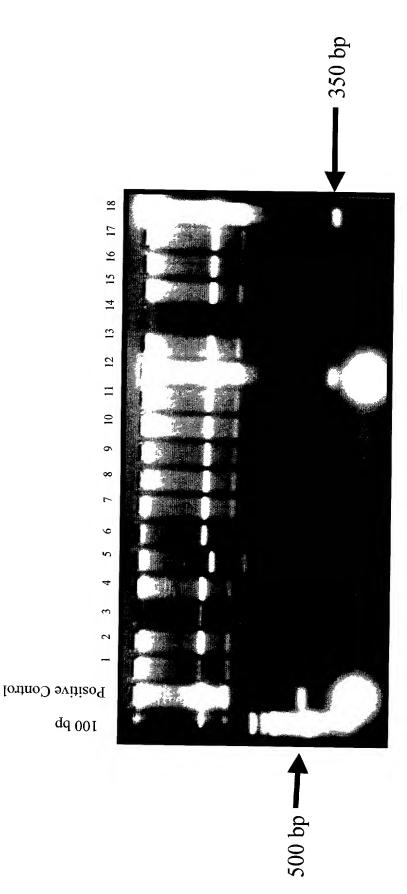
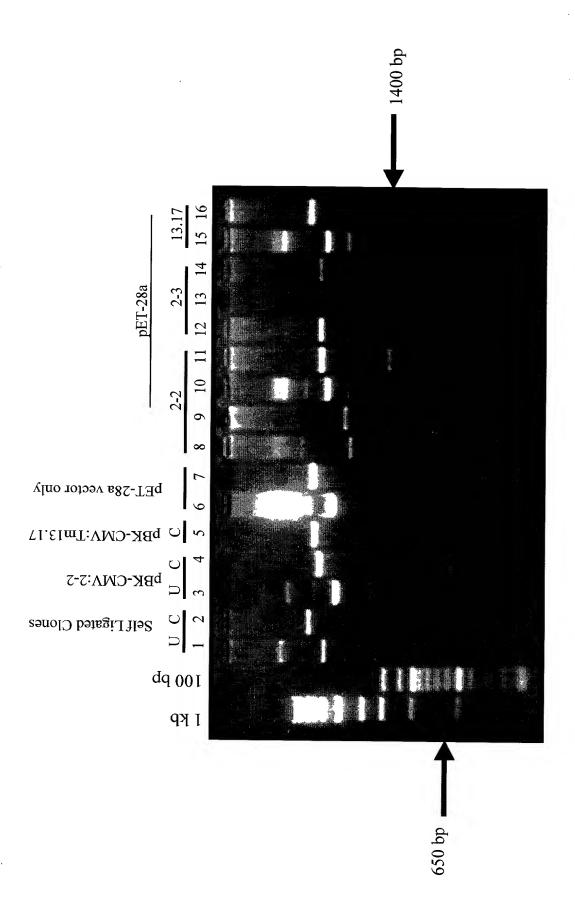
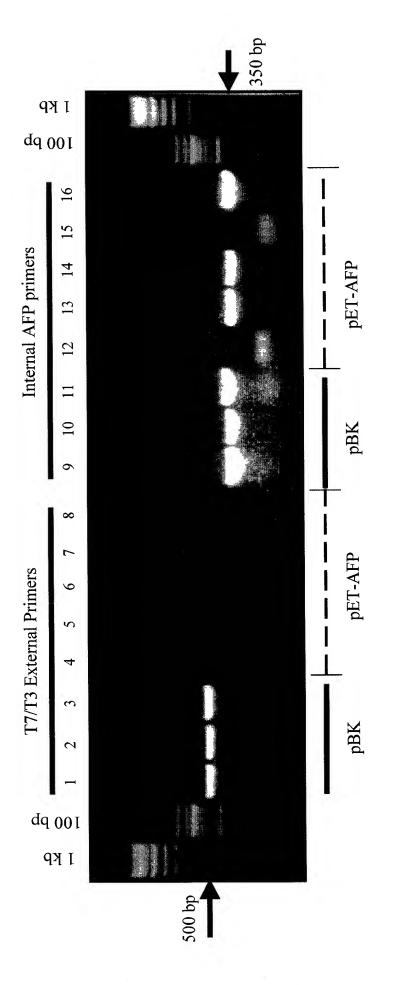


Fig. 5.2





Hig. 5.4

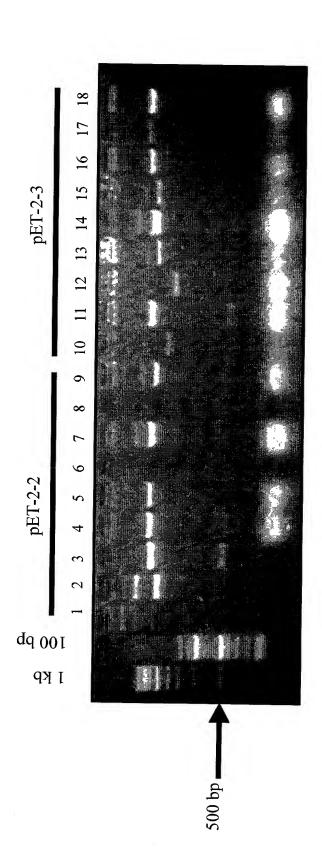


Fig. 5.5

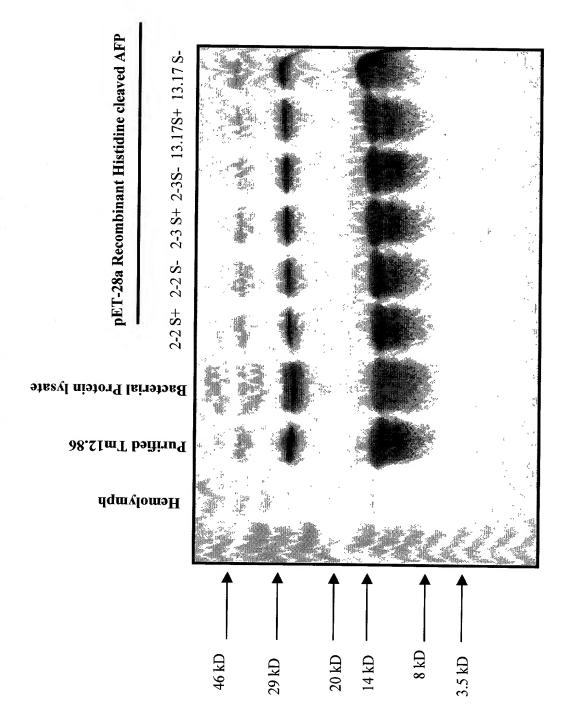


Fig 5.6

#### His-tagged Clone 2.2 with signal sequence

TTGTTAGCGG ATGGAATTCC CTCGTAGGGG ATAATTTTGT TTACTTTAAG	50
His-tag Start Codon  AAGGAGATAT ACC ATG GGC AGC AGC CAT CAT CAT CAT CAC AGC  Met Gly Ser Ser His His His His His His Ser  -55 -50	96
AGC GGC CTG GTG CCG CGC GGC AGC CAT ATG GCT AGC ATG ACT GGT Ser Gly Leu Val Pro Arg Gly Ser His Met Ala Ser Met Thr Gly -45 -40 -35	141
AFP Start GGA CAG CAA ATG GGT CGC GGA TCC GAA TTC GCA CGA GCA AAA ATG GJy Gln Gln Met GJy Arg GJy Ser GJu Phe Ala Arg Ala Lys Met -30 -25 -20	Codon 186
AAA CTC CTC TTG TGC TTT GCG TTC GCC GCC ATC GTC ATC GGA GCT  Lys Leu Leu Cys Phe Ala Phe Ala Ala Ile Val Ile Gly Ala  -15 -10 -5	231
N-terminal of mature AFP CAG GCT CTC ACC GAC GAA CAG ATA CAG AAA AGG AAC AAG ATC AGC $\frac{G\ln Ala}{1}$ Leu Thr Asp Glu Gln Ile Gln Lys Arg Asn Lys Ile Ser $\frac{G\ln Ala}{1}$	276
AAA GAA TGC CAG CAG GTG TCC GGA GTG TCC CAA GAG ACG ATC GAC Lys Glu Cys Gln Gln Val Ser Gly Val Ser Gln Glu Thr Ile Asp 15 20 25	321
AAA GTC CGC ACA GGT GTC TTG GTC GAT GAT CCC AAA ATG AAG AAG Lys Val Arg Thr Gly Val Leu Val Asp Asp Pro Lys Met Lys Lys 30 35 40	366
CAC GTC CTC TGC TTC TCG AAG AAA ACT GGA GTG GCA ACC GAA GCC His Val Leu Cys Phe Ser Lys Lys Thr Gly Val Ala Thr Glu Ala 45 50 55	411
GGA GAC ACC AAT GTG GAG GTA CTC AAA GCC AAG CTG AAG CAT GTG Gly Asp Thr Asn Val Glu Val Leu Lys Ala Lys Leu Lys His Val 60 65 70	456
GCC AGC GAC GAA GAG GTG GAC AAG ATC GTG CAG AAG TGC GTG GTC Ala Ser Asp Glu Glu Val Asp Lys Ile Val Gln Lys Cys Val Val 75 80 85	501
AAG AAG GCC ACA CCA GAG GAA ACG GCT TAT GAC ACC TTC AAG TGT Lys Lys Ala Thr Pro Glu Glu Thr Ala Tyr Asp Thr Phe Lys Cys 90 95 100	546
Stop Codon ATT TAC GAC AGT AAA CCT GAT TTC TCT CCT ATT GAT TAA TTGTTTTGTA Ile Tyr Asp Ser Lys Pro Asp Phe Ser Pro Ile Asp * 105 110 115	595
Polyadenylation signal Poly-A tail TTTGACTGAA TTTTGAC <u>AAT AAA</u> GGTAATA TCGTTATGTA AAAAAAAAAA	645
AAAAAACTCG AGCACCACCA CCACCACCAC TGAGAT	681

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TTG	TTAG	CGG	ATGG	AATT	CC C	TCGT	AGGG	G AT	AATT	TTGT	TTA	CTTT	AAG		50
AAG	GAGA	TAT	ACC	His- ATG Met	GGC	AGC .	AGC	CAT	CAT His	CAT His	CAT His	CAT His	CAC His -25	AGC Ser	96
AGC Ser	GGC Gly	CTG Leu	GTG Val -20	CCG Pro	CGC Arg	GGC Gly	AGC Ser	CAT His -15	Met	GCT Ala	AGC Ser	ATG Met	ACT Thr -10	GGT Gly	141
GGA Gly	CAG Gln	CAA G1n	ATG Met -5	GGT Gly	CGC Arg	GGA Gly	TCC Ser	CTC	ermi ACC Thr	GAC	GAA	CAG	ATA	CAG	186
AAA Lys	AGG Arg	AAC Asn 10	AAG Lys	ATC Ile	AGC Ser	AAA Lys	GAA Glu 15	TGC Cys	CAG Gln	CAG Gln	GTG Val	TCC Ser 20	GGA Gly	GTG Val	231
TCC Ser	CAA Gln	GAG G1u 25	ACG Thr	ATC Ile	GAC Asp	AAA Lys	GTC Val 30	CGC Arg	ACA Thr	GGT Gly	GTC Val	TTG Leu 35	GTC Val	GAT Asp	276
GAT Asp	CCC Pro	AAA Lys 40	ATG Met	AAG Lys	AAG Lys	CAC His	GTC Val 45	CTC Leu	TGC Cys	TTC Phe	TCG Ser	AAG Lys 50	AAA Lys	ACT Thr	321
GGA Gly	GTG Val	GCA Ala 55	ACC Thr	GAA Glu	GCC Ala	GGA Gly	GAC Asp 60	ACC Thr	AAT Asn	GTG Val	GAG Glu	GTA Val 65	CTC Leu	AAA Lys	366
GCC Ala	AAG Lys	CTG Leu 70	AAG Lys	CAT His	GTG Val	GCC Ala	AGC Ser 75	GAC Asp	GAA G1u	GAG G1u	GTG Val	GAC Asp 80	AAG Lys	ATC Ile	411
GTG Val	CAG G1n	AAG Lys 85	TGC Cys	GTG Val	GTC Val	AAG Lys	AAG Lys 90	GCC Ala	ACA Thr	CCA Pro	GAG G1u	GAA G1u 95	ACG Thr	GCT Ala	456
TAT Tyr	GAC Asp	ACC Thr 100	TTC Phe	AAG Lys	TGT Cys	ATT Ile	TAC Tyr 105	GAC Asp	AGT Ser	AAA Lys	CCT Pro	GAT Asp 110	TTC Phe	TCT Ser	501
			TAA	CTCG		ICC A	CCAC	CACC	CA CC	CACTO	AGAT				543

His-tagged clone 2.3 with signal sequence	
TTGTTAGCGG ATGGAATTCC CTCGTAGGGG ATAATTTTGT TTACTTTAAG	50
His-tag Start Codon  AAGGAGATAT ACC ATG GGC AGC AGC CAT CAT CAT CAT CAC AGC Met Gly Ser Ser His His His His His Ser -55 -50	96
AGC GGC CTG GTG CCG CGC GGC AGC CAT ATG GCT AGC ATG ACT GGT Ser Gly Leu Val Pro Arg Gly Ser His Met Ala Ser Met Thr Gly -45 -40 -35	141
GGA CAG CAA ATG GGT CGC GGA TCC GAA TTC GCA CGA GCA AAA ATG Gly Gln Gln Met Gly Arg Gly Ser Glu Phe Ala Arg Ala Lys Met -30 -25 -20	rt Codo 186
AAA CTC CTC TTG TGC TTT GCT TTC GCC GCC ATC GTC ATC GGA GCT Lys Leu Leu Cys Phe Ala Phe Ala Ala Ile Val Ile Gly Ala -15 -5	231
N-terminal of Mature AFP CAG GCT CTC ACC GAC GAA CAG ATA CAG AAA AGG AAC AAG ATC AGC Gln Ala Leu Thr Asp Glu Gln Ile Gln Lys Arg Asn Lys Ile Ser $1$ 5 10	276
AAA GAA TGC CAG CAG GTG TCC GGA GTG TCC CAA GAG ACG ATC GAC Lys Glu Cys Gln Gln Val Ser Gly Val Ser Gln Glu Thr Ile Asp 15 20 25	321
AAA GTC CGC ACA GGT GTC TTG GTC GAT GAT CCC AAA ATG AAG AAG Lys Val Arg Thr Gly Val Leu Val Asp Asp Pro Lys Met Lys Lys 30 35 40	366
CAC GTC CTC TGC TTC TCG AAG AAA ACT GGA GTG GCA ACC GAA GCC His Val Leu Cys Phe Ser Lys Lys Thr Gly Val Ala Thr Glu Ala 45 50 55	411
GGA GAC ACC AAT GTG GAG GTA CTC AAA GCC AAG CTG AAG CAT GTG GJy Asp Thr Asn Val Glu Val Leu Lys Ala Lys Leu Lys His Val 60 65 70	456
GCC AGC GAC GAA GAA GTG GAC AAG ATC GTG CAG AAG TGC GTG GTC Ala Ser Asp Glu Glu Val Asp Lys Ile Val Gln Lys Cys Val Val 75 80 85	501
AAG AAG GCC ACA CCA GAG GAA ACG GCT TAT GAC ACC TTC AAG TGT Lys Lys Ala Thr Pro Glu Glu Thr Ala Tyr Asp Thr Phe Lys Cys 90 95 100	546
Stop Codon ATT TAC GAC AGT AAA CCT GAT TTC TCT CCT ATT GAT TAA TTGTTTTGTA Ile Tyr Asp Ser Lys Pro Asp Phe Ser Pro Ile Asp * 105 110 115	595
Polyadenylation signal Poly-A tail TTTGACTGAA TTTTGACAAA AAAGGTACTA TCGTTATGAA AAAAAAAAA	645
AAAAAAACTC GAGCACCACC ACCACCACCA CTGAGAT	682

His-	tago	ged C	lone	2.3	3 wit	hout	; sig	ına 1	sequ	ience	9				
TTGT	TTAGO	CGG A	ATGGA	ATTO	CC CT	CGTA	\GGGG	aTA	WTTT	TGT	TTAC	CTTTA	<b>V</b> AG		50
AAG(	GAGAT	TAT A	ACC A	ATG G	agč <i>i</i>	AGC A	Ser F	CAT				is F			96
		CTG Leu													141
		CAA Gln						CTC	ACC	GAC	GAA		ATA	CAG	186
		AAC Asn 10													231
		GAG G1u 25													276
		AAA Lys 40													321
		GCA Ala 55													366
		CTG Leu 70													411
		AAG Lys 85													456
		ACC Thr 100													501
		GAT Asp	TAA	CTC(		ACC A	ACCA(	CCAC	CA CO	CACTO	gaga ⁻	Γ			543

His-tagged Tm 13.17 with signal sequence	
TTGTTAGCGG ATGGAATTCC CTCGTAGGGG ATAATTTTGT TTACTTTAAG	50
His-tag Start Codon  AAGGAGATAT ACC ATG GGC AGC AGC CAT CAT CAT CAT CAC AGC  Met Gly Ser Ser His His His His His Ser  -65  -60  -55	96
AGC GGC CTG GTG CCG CGC GGC AGC CAT ATG GCT AGC ATG ACT GGT Ser Gly Leu Val Pro Arg Gly Ser His Met Ala Ser Met Thr Gly -45 -45	141
GGA CAG CAA ATG GGT CGC GGA TCC GAA TTC TGG ATC CAA AGA ATT Gly Gln Gln Met Gly Arg Gly Ser Glu Phe Trp Ile Gln Arg Ile -35 -30 -25	186
AFP Start Codon  CGG CAC GAG ACT ACT AAG ATG AAG TTG CTC TGT TGT CTA ATC TCC  Arg His Glu Thr Thr Lys Met Lys Leu Leu Cys Cys Leu Ile Ser  -20 -15 -10	231
N-terminal of mature AFP CTC ATT CTG TTG GTC ACA GTT CAG GCC CTG ACC GAG GCA CAA ATT Leu Ile Leu Val Thr Val Gln Ala Leu Thr Glu Ala Gln Ile -5 1 5	276
GAG AAA CTG AAC AAG ATC AGC AAA AAA TGT CAA AAT GAA AGT GGA Glu Lys Leu Asn Lys Ile Ser Lys Lys Cys Gln Asn Glu Ser Gly 10 15 20	321
GTG TCG CAA GAG ATC ATA ACC AAA GCT CGC AAC GGT GAC TGG GAG Val Ser Gln Glu Ile Ile Thr Lys Ala Arg Asn Gly Asp Trp Glu 25 30 35	366
GAC GAT CCT AAA CTG AAA CGC CAA GTT TTT TGC GTG GCC AGG AAC Asp Asp Pro Lys Leu Lys Arg Gln Val Phe Cys Val Ala Arg Asn 40 45 50	411
GCC GGT CTG GCC ACG GAA TCG GGA GAG GTG GTG GTC GAC GTG TTG Ala Gly Leu Ala Thr Glu Ser Gly Glu Val Val Val Asp Val Leu 55 60 65	456
AGG GAG AAG GTG AGG AAG GTC ACT GAC AAC GAC GAA GAA ACT GAG Arg Glu Lys Val Arg Lys Val Thr Asp Asn Asp Glu Glu Thr Glu 70 75 80	501
AAA ATC ATC AAT AAG TGC GCC GTC AAG AGA GAT ACT GTT GAA GAG Lys Ile Ile Asn Lys Cys Ala Val Lys Arg Asp Thr Val Glu Glu 85 90 95	546
ACG GTG TTC AAT ACT TTC AAA TGT GTC ATG AAA AAC AAG CCA AAG Thr Val Phe Asn Thr Phe Lys Cys Val Met Lys Asn Lys Pro Lys 100 105 110	595
Stop Codon TTC TCA CCA GTT GAT TGA ACCACCACGA CTAGTAGATG GTTCAAATGG Phe Ser Pro Val Asp * 115	643
Polyadenylation signal Poly-A tail TGTGCTTTAC ATATAAAAAA AAAGTGTTTC TGATGTAAAA AAAAAAAAAA	693
AAAAAAAAA AACTCGAGAG TATTCTAGAG CGGCCGCGGG CCCATCGTTT	743
TCCACCCCTC GAGCACCACC ACCACCACCA CTGAGAT	777

His-	tagg	ged T	m 13	3.17	with	nout	sigr	nal s	eque	ence				
TTGT	TAGO	CGG A	TGGA	WTTO	с ст	CGTA	\GGGG	ATA	\ATT1	TGT	TTAC	CTTTA	AAG	50
AAGG	GAGAT	FAT A	ACC A	ATG 0	ag S GC A Ny S	AGC A Ser S	AGC (	CAT (			11s F			96
		CTG Leu -20												141
		CAA Gln -5					CTG	ACC	GAG		CAA	ATT	GAG	186
		AAG Lys												231
		ATC Ile												276
		CTG Leu												321
		ACG Thr								Asp				366
		AGG Arg												411
		AAG Lys												456
		ACT Thr												 501
		GAT Asp	TGA	CTC(		ACC A	ACCA(	CCAC	CA CO	CACTO	GAGAT	Γ		543

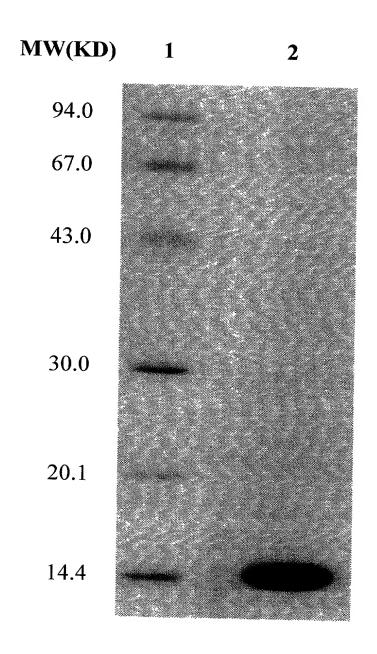


Fig. 6.0

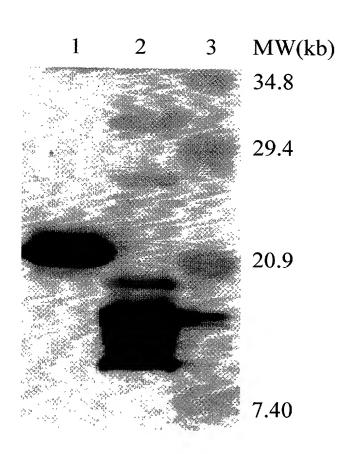


Fig. 6.1

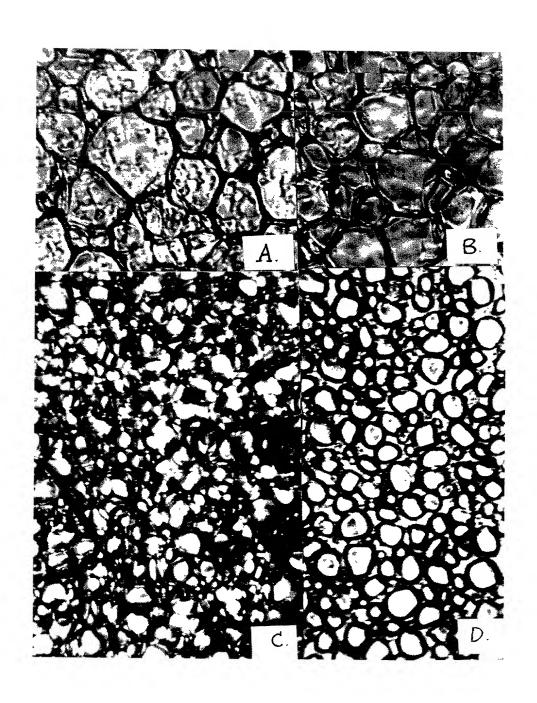
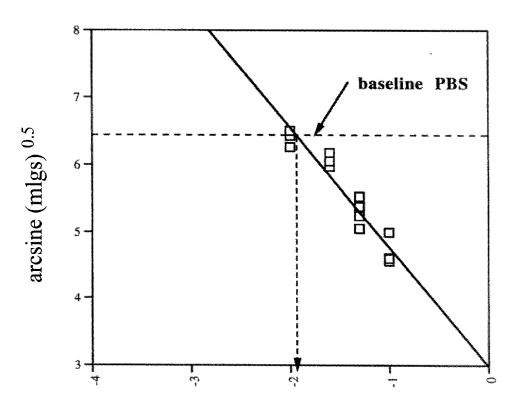


Fig. 6.2

Tm 13.17 S-graph data



log dilution

ONE LETTER	NAME	THREE LETTER	CHEMICAL CLASS	HYDROPHOBICITY	Reactivity
Α	Alanıne	Ala	aliphatic	mod. hydrophobic	low
В	Asp or Asn	Asx	•	•	
С	Cysteine	Cys	sulfhydryl	hydrophobic	high
D	Aspartic Acid	Asp	acidic	highly hydrophilic	high
E	Glutamic Acid	Glu	acidic	highly hydrophilic	high
F	Phenylalanine	Phe	aromatic	highly hydrophobic	low
G	Glycine	Gly	aliphatic	mod. hydrophobic	low
Н	Histidine	His	basic, imidazole	highly hydrophilic	high
1	Isoleucine	lle	aliphatic	hydrophobic	low
J			•	,	
K	Lysine	Lys	basic	highly hydophilic	high
L	Leucine	Leu	aliphatic	hydrophobic	low
M	Methionine	Met	sulfhydryl	hydrophobic	low
N	Asparagine	Asn	amide, acidic derived	hydrophilic	high
0	_		•	, ,	9
₽	Proline	Pro	aliphatic, cyclic, imino	mod. hydrophilic	low
Q	Glutamine	Gln	amide, acidic derived	hydrophilic	high
R	Arginine	Arg	basic	highly hydrophilic	high
S	Serine	Ser	aliphatic hydroxyl	hydrophilic	high
T	Threonine	Thr	aliphatic hydroxyl	hydrophilic	high
U			, , , .	муш ориш о	9
V	Valine	Val	aliphatic	hydrophobic	low
W	Tryptophan	Trp	aromatic	highly hydrophobic	low
X		•			
Υ	Tyrosine	Tyr	aromatic	mod. hydrophilic	high
Z	Glu or Gln	Gĺx			9
		ACD	Any Acidic		
		ALP	Any Aliphatic		
		ALH	Any Aliphatic Hydroxyl		
		ARO	Any Aromatic		
		BAS	Any Basic		
		HY-	Hydrophobic		
		HY+	Hydrophilic		

Position	Tm12 84-2 2	Tm12 84-2 3	Tm12 84-3 4	Tm12 84-3 9	Tm12 84-7 5	Concensus of	Tm13 17	Concensus with	B1	Concernsus with	AFP-3	Concensus with
1	A	A	A	A	A	Tm12 84 A	A	Tm 13 17 A		81 A	C	. AFP-3- N ~ N
2 3	C G	C G	C G	C G	C G	C G	G A	N R		N R	A G	R
4 5	A G	A G	A G	A G	A G	A G	C T	N N		N	A T	N N
6 7	C A	C A	C A	C A	C A	C A	A C	N N		N N	C	N N
8	A	A	A	A A	A A	A	T A	N A		N A	G A	N A
10 11	A A	A	A	A A	A A	A	A G	A R		A R	A G	A R
12 13	A A	Α .	A	A	A	A	• A	A	A?	A	A	Ā
14 15	T G	T G	T G	T G	T G	T G	T G	T G	T? G?	T G	T G	т G
16 17	A A	Ā	Ā	Ā	Ā	A A	A A	A		A A	A A	A
18 19	Â	Ã	Ã	Ã	Ã	A C	Ğ	R Y		R Y	G	R Y
20	T	Ŧ	т	τ	T	T	† G	r c/G		Ť C/G	T C	T C/G
21 22	c	c	c	c	ç	C C	Ċ	Ç		С	С	C T
23 24	Č.	Č.	C C	Č.	Č.	Č.	T C	ċ		T C	C C	Ċ Y
25 26	Ť	7	T T	T T	T T	Ţ	T G	T N		T N	C T	N
27 28	G T	G T	G T	G T	G T	G T	T T	N T		N T	C T	N T
29 30	G C	G C	G C	G C	G C	G C	G T	G Y		G Y	G T	G Y
31 32	T T	T T	T T	T T	T T	T T	C T	Ť	C T	Ť	C T	Ť
33 34	T G	T G	T G	T G	T G	T G	A A	T/A R	T A	T/A R	T G	T/A R
35 36	Ċ G	Ċ T	Ċ	C T	C G	C N	T C	Y N	C T	Y N	T C	Y N
37 38	Ť	Ť Ť	Ť	Ť	Ť	T	T C	Ţ	T C	T Y	C T	Y Y
39 40	G	Ċ	Ċ	c G	Ċ	Ċ G	Ċ	G/C C	T C	Ý G/C	C G	Ý G/C
41 42	c	c c	c c	Ċ	o c	Ċ	T C	Y C	T C	Y C	Ť	Y
43	G	G	G	G	G	G	A T	Ř Y	Ā	R Y	G	Ř Y
44 45	c c	c	C C	C	c	c	т	Ý	Ť C	Ý N	C C T	N
46 47	A T	A T	A T	A T	A T	A T	C T	N T	т	т	Т	т
48 49	C G	C G	C G	C G	C G	G G	G T	C/G N	G T	C/G N	G G	C/G N
50 51	T C	T C	T C	T C	T C	T C	T G	T C/G	T G	T C/G	r c	T C/G
52 53	A T	A T	A T	A T	A T	A T	G T	R T	G T	R T	G C	R Y
54 55	C G	C G	C G	C G	C G	C G	C A	C R	c	C N	C G	C N
56 57	G A	G A	G A	G A	G A	G A	C A	G/C A	C A	G/C A	C G	G/C R
58 59	G C	G C	G C	G	G C	G	G T	G Y	G T	G Y	A C	R Y
60 61	T C	Ť C	T C	T C	T C	T C	T C	C C	T C	T C	C T	Y Y
62 63	A G	A G	A G	Ā G	A G	A G	A G	A G	A G	A G	A C	A N
64 65	Ğ	Ğ	G C	G	Ğ	G C	Ġ	G C	G C	G C	G	G C
66 67	T C	T C	T C	Ť C	Ť C	Ť C	c	Ý C	C A	Y N	С	Y N
68 69	T C	T C	T C	T C	Ť C	Ť	T G	T C/G	T A	T N		T N
70	Ä	Ã	Ä	Ã	Ä	A C	Ā	A C	A	A C		A C
71 72 73	č	Č G	č	č	č	č	Ċ	Ċ	Ť	G/C	G	GIC Y
74	A C	A	A C	A T	A C	Ã	A G	A N	A G	A N	A	A N
75 76	G	G	G	Ġ	Ğ	Ġ	Ğ	G N	G A	G N	Ä	R N
77 78	A A	A	A A	A	Α	A A C	A	A C	Ā	A C/G	Ā	A C/G
79 80	C A	C A	C A	C A	C A	Ā	A A	A R	A	A N	ç	N N
81 82	G A	G A	G A	G A	G A T	Ā	Ä	Â	C T	N T	Ċ	N N
83 84	T A	T A	T A	T A	Ä	Å	Ť	A/T C/G	Ť G	A/T C/G	Ť G	A/T C/G
85 86	C A	C A	C A	C A	C A	C A	G A	A	Α	A	A	Α
87 88	G A	G A A A G	G A	A	A	G A A	G A A C T	G A A N	Ċ	G N	G A A G C T	G N
89 90	A A	A	A A	A A	A	A	A	A A	Å	&\ a	G	R
90 91 92	A G	A G	A G	A G	A G	A G	C T	N N	Ť	N N	Ţ	N N
93 94 95 96 97 98	G A	G A	G A	G A	G A	G A	G A	G A	G C	G N	G A	G N
95 96	A C	A C	A C	A C	A C	A C	A A C	A C	c	N C	A G	N Y
97 98	A A	A A	A A	A A	A A	A A	A A G	A A	C A	N A	C A	N A
99	G A	G A	G A	G A	G A	G A	G A	N G A A C A A G A T C A G C	A	R A	G C	R N
100 101 102	T C	T C	T C	T C	T C	T C	A T C	T C	c	Y C	A C	N C
103	Ā	A G	A G	A G	A G	A G	A G C	A G	A G	A G	A G	A G
104 105	č	č	č	č	Č A	Č A	Č A	C A	c G	C R	C G	C R
106 107 108	Ä	Â	Ã	Â	Ã	Ä	Ã A A	A A R	Č.	N A	Ā	N N
109	Ğ	Ĝ	Ğ	Ğ	Ğ	Ĝ	Ä	Ŕ	Ğ	Ŕ	Ğ	R N
110 111	G A A A A G G A A C A A G A T C A G C A A A G A A T	Ā	Ą	Ą	Ğ	R T	Ā	A R T	Ĝ	Ŕ	Ç	Ņ T
112 113 114	G	Ğ	G	ė.	Ğ	Ġ	Ġ	Ġ Y	Ġ	Ġ	Ģ.	\$ r z z g z z y z a r z z c a g c r z z r z z t g y
115	G C C A G	G A A C A A G A T C A G C A A A A C A A T G C C A G	G A A A A G G A A C A A G A T C A G C A A A G A A T G C C A G	G A A A A G G A A C A A G A T C A G C A A A G A A T G C C A G	G A A A A G G A A C A A G A T C A G C A A A G A G T G C C A G	A G G A A C A A G A T C A G C A A A G A R T G C C A G	G T C	С	G C T A C T G C C C C A A A C C A G C G C G C A G A G	ARAYCAGCRNARARIGYNAR	A A G C A G C A G C G A C G C C T G C A A G	N A R
116 117	A G	A G	A G	A G	A G	G G	A	A R	Ğ	R	Ğ	R

102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102   102	Position	Tm12 84-2 2	Tm12 84-2 3	Tm12 84-3 4	Tm12 84-3 9	Tm12 84-7 5		Tm13 17	^			AFP-3	
90 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	118	С	С	С	С	С		Α		B1 A		G	
100   10   10   10   10   10   10   10	120	G	G	G	Ĝ	Ĝ	G	T	N	τ	N	т	N
101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101   101	122	T	T	T	A	T	T/A	A	T/A	A	TIA	A	A/T
100   0   0   0   0   0   0   0   0   0	124	T	Ť	T	T	т	T	A	T/A	A	TIA	Т	TIA
98	126	С	С	С	С	С	С	Т	Y	T	Y	Т	Y
100   0   0   0   0   0   0   0   0   0	128	G	G	G	G	G	Ğ	G	G	G	G	G	G
00 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	130	G	G	G	G	G	G	G	G	G	G	G	G
1941   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195   195	132	G	G	G	G	G	Ġ	Ģ	Ġ	Ġ	G	Á	R
1989 C C C C C C C C C C C C C C C C C C	134	Ċ	С	С	C	C	C	c	C	C	C	C	C
188 A A A A A A A A A A A A A A A A A A	138	C	С	С	Ċ	C	Ċ	Ċ	С	G	C/G	Ġ	C/G
100   A	138	A	A	Α	Α	Α	Α	Α	A	A	A	A	A
143	140	A	A	Α	A	Α	Α	Ä	A	A	A	À	A
1444 Q G G G G G G G G G G G G G G G G G	142	Α	A	A	A	Α	A	A	A		R		N
1861 T T T T T T T T T T T T T T T T T T T	144	G			Ġ	G			G/C				G/C
1484	146	Ŧ	A T	A T	A T	A T			A T				
140													
161 A A A A A A A A A A A A A A A A A A	150	A C	A C		A	Α	A	c	N		N	A	N
Section   Sect									A A		A		A
185	153 154	A	A	Α	Α	Α	A	A	A	Α	Α	G	R
157 G C C C C C C C C C C C C C C C C C C	155	T		Т		T		С	Υ	C	Υ	Т	Υ
1869		С	C	C	C	С	C	C	С	c	С	С	Ċ
He   C	159	C	C		Ċ		c	C	С	С	С	c	c
1816   Q	161	С	С	C	c	c	c	A	N	A	N	Α	N
1869				G	G	G	G	G	G	G	G	C	G/C
187	165	T	Т	T	T	Т	т	т	7	T	T	T	T
1890	167	T	т	T	T	т	T	Α	TIA	A	T/A	A	T/A
171	169	7	T	T	т	T	Т	Т	T	T	T	G	N
173	171	G	G	Ġ	G	G	G	G	G	G	G	Α	R
176	173	Т	Т	т	T	т	T	A	TIA	A	T/A	T	T/A
177	175	G	G	Ğ	G	G	G	G	G	G	G	G	G
176	177	T	C	С	C	С	Y	c	Y	C	Y	C	Y
181	179	A	Α	Ā	Α	Α	A	Α	Α	A	A	Α	Α
183	181	С	C	С	Ç	С	С	c	C	C	c	C	Ċ
185 A A A A A A A A A A A A A A A A A A A	183	С	С	С	C	С	Ċ	Т	Υ	С	Y	C	Υ
187	185	Α	Α	Α	A	Α	A	A	A	A	A	A	Α
189	187	Α	A	A	A	A	A	c	N	С	И	C	N
191 A A A A A A A A A A A A A A A A A A	189	G	G	G	G	G	G	G	G	G	G	G	G
1993 A A A A A A A A A A A A A A A A A A	191	A	Α	A	Α	Α	Α	Α	Α	A	A	Α	A
1995 G G G G G G G G G G G G G G G G G G	193	A	Α	Α	A	A	A	c	N	Α	N	G	N
197 A A A A A A A A A A A A A A A A A A A	195	G	G	G	G	G	G	С	G/C	G	G/C	G	G/C
199 G G G G G G G G G G G G G G G G G G	197	A	A	Α	Α	Α	A	A	Α	A	Ā		A
201	199	G	G	G	G	G	G	G	G	c	G/C		G/C
203	201	C	С	C	c	C	С	T	Y	Ť	Ý		Y
205	203	T	T	Т	T	T	T	T	T	т	Т	ť	т
207	205	T	T	т	Ť	T	Т	Т	T	T	Ť	τ	т
210	207												
111	209	Ť	Ť	Ť	į	Ť	Ť	Ţ	T	Ĵ	T	Ť	Ť
113	211	Ť	Ť	Ŧ	T	Υ	T	Ğ	N	Ţ	N	Ť	Ň
215 A A A A A A A A A A A A A A A A A A A	213	Ğ	Ğ	G	G	G	G	Ç	Gic	ć	G/C	Ġ	GIC
217 A A A A A A A A A A A A A A A A A A A	215	A	Ä	Â	A	Ä	Ä	Ĝ	R	Â	Ŕ	Ä	Ŕ
219 A A A A A A A A A A A A A A A A A A A	217	Ā	Ā	Ā	A	Ä	A	Ā	A	G	R	Ā	R
221		Ā	Â	Ā	A	A	A	ć	N	Ä	N N	A	N
-222	221	Ĝ	ç	Ĉ	Ĉ	Ĉ	ç	c	Ċ	ř	Y	900	Y V
225	223	Ġ	Ġ	Ġ	G	G	G	G	Ğ	G	G	J G C	Ğ
2277 J J J J J J J J J J J J J J J J J J	225	A	A	A	A	A	A	T	AVT	Ä	A,T	Ā	AT
229 G G G G G G G G G G G G G G G G G G	227	ĭ	7	ĭ	Ţ	T	Ţ	Ţ	Ţ	Ť	T E	Ť	T L
201 A A A A A A A A A A A A A A A A A A A	229	9 0	9	Ģ	G	9	G	G	G	Ĝ	G G	Ą	R C
233 C C C C C C C C C A N 234 C C C C C C G C/G G C/G 235 G G G G G G G G G	231	Ä	Ä	A	A	A	A	Ç	N.	c c	ŭ	С	N
235 G G G G G G G G G	233	ő	ć	Ĉ	Č.	C	C	C	C C	o c	× C	G A	N N
	235	Ğ	G	Ğ	G	Ğ	Ğ	G	G	G	G	G	G

Fig. 7.2 cont.

Position	Tm12 84-2 2	Tm12 84-2 3	Tm12 84-3 4	Tm12 84-3 9	Tm12 84-7 5	Concensus of	Tm13 17	Concensus with	B1	Concensus with	AFP-3	Concensus with
236 237	A A G			A A	A A	A A	A A	A A	Α	A A	C C	N N
238 239	G	A G C	A A G C	G	G	G C	T C	N C	A T C	Ñ C	A G	N C/G
240 241	CCG	Ċ G	C G	C G	Ċ G	Ċ G	Ğ	c <i>i</i> G G	G	CIG	T	N G
242 243	G	G A	G A	G A	G A	Ğ A	G A	G A	G G A	G G A	G G T	Ğ A/T
244 245	A G A	Ĝ A	G A	G A	Ĝ	Ĝ	Ĝ	Ĝ	G	G	G	G
246 247	С	С	С	Ĉ A	С	c	G	C/G	Ą	A N	Ą	A N
248 249	A C C	A C C	A C C	ĉ	A C C	A C C	G T	R Y C/G	A T T	R Y	T T	N Y
250 251	Α	A	A	Α	A	A	G G	R	G	N R	ç	N N
252 253	A T G	A T G	A T G	A T G	A T G	A T G	T G G	A/T N G	A G G	AT N	A	A/T N
254 255	T G	Ť G	Ť G	T G	T G	ī G	T	T G/C	C	G Y	C	G/C Y
256 257	Ğ A	G A	G A	G A	G A	G A	C G A	G A	G	G/C G	G	G/C G A
258 259	Ğ	Ğ	Ğ	Ğ	Ğ	Ğ G	c	GIC	A C	G/C	A C	G/C N
260 261	T A	T A	T A	T A	T A	T A	G T	G T R	A C	R Y	C A C	N
262 263	Ĉ T	Ĉ T	Č T	Ĉ T	Ĉ T	Ĉ T	G T T	Y T	G T T	R Y T	A T	N N T
264 265	C A	Ċ A	Ċ A	C A	Ċ	Ċ A	G A	c <i>i</i> G A	Ċ A	C/G A	т	N A
266 267	A	Ā	A A	A A	Ä	A A	Ğ	R R	Ã G	Ř Ř	A A G	Ř R
268 269	A G C	Ĝ	Ğ	Ĝ	Ğ	Ĝ	G A	G N	G A	G N	A	R N
27 <b>0</b> 271	Č A	C A	Č A	C A	C A	Č A	Ğ A	c/G A	Ĝ	C/G	G	CIG
272 273	Α	Ã G	A G	Ā	Ã	Â G	Ā	Ã	Α	A	A	A A
274 275	G C T	C T	C	C	C	C	G T	c/G T	G	G N T	A T	R N T
276 277	G A	Ġ	Ġ A	Ġ A	G A	G A	Ġ A	Ġ	G A	G	T C	G/C
278 279	A G	Â G	A G	Ā	Ã	Ã	Ğ	R G	Ċ	A N G	A A G	A N G
280 281	C A	C A	C A	C A	Č A	C A	Ā	N A	A G	N R	G A	N R
282 283	T G	T G	Ť G	Ť G	Ť G	Î G	Ĝ	Ñ G	G	N N	Α	N
284 285	G G	Ť	ř	T G	T G	ī G	T C	T G/C	G A	N N	A A	N N N
286 287	G C	G	G C	Ğ	Ğ	Ğ	Â	R C	Ĉ	N N	C T	N
288 289	Č A	C A	C A	Č A	Č A	Č A	Ť G	Ř	A A	N R	C T G	N N R
290 291	Ĝ	e c	Ĝ	Ĝ	Ğ	Ĝ	Ā	R C	Č	N C/G	A	N
292 293	Ü	Ŭ	Ŭ	Ü	•	·	Ä	Ä	A T	A A/T	G G A	C/G R A/T
294 295	G	G	G	G	G	G	Ĉ	Ĉ	G	C/G	Ť Ť	N N
296 297	Ã	A C	A C	Ã	A C	A C	Á	A	A T G	R A/T C/G	c G	N C/G
298 299	G A	Ğ	G A	Ğ A	Ğ	Ğ	Ğ A	Ğ A	A A	R A	G A	R A
300 301	A G	Ã G	A G	Ā	Ä	Â	Ã	Â	Ğ	R R	Ğ	R R
302 303	A G	Ā	A G	A A	A G	A R	A A	A R	Ä	A R	A G	A R
304 305	Ğ	G T	Ğ	G T	Ğ	Ğ	Â	R Y	Ĝ	Ŕ	G	R Y
306 307	G G	G	G G	Ġ	G	G	T G	N G	Ğ	N R	Č G	N R
308 309	A C	Ä	A C	Ä C	A C	A C	Ā	A C/G	Ğ	R N	Ā	R
310 311	Ä A	Ā	Ā	Ā	A A	A A	Ā	A A	Ä G	A R	Ġ A	R R
312 313	G A	G A	G A	G A	G A	G A	Â	R A	Ā	R	Ĉ	N
314 315	T C	T	T C	T C	T C	T C	T C	Ť	Ť	A/T T C/G	Ţ G	A/T T C/G
316 317	G T	G T	G T	G T	G T	G T	Ā	Ŕ T	T C	N Y	Ğ	N Y
318 319	G C	G	Ģ C	G C	G C	G	C A	G/C N	G A	G/C N	Ğ	N N
320 321	A G	A G	A G	A G	A G	A G	A T	A N	G A	R N	C	N N
322 323	A A	A A	A A	A A	A A	A A	A A	A A	A G	A R	A	A R
324 325	G T	G	G T	G	G	G	G	G	T	N	A	KI.
326 327 328	G C	C	C G	G C	G C	G C	G C	T G C G Y G G T C A A G A R R	C A	N G/C N G/C N	G	N G/C N G/C N
329	G T	G T	G G	G T	G T	G T	G C	G Y	C G	G/C N	G C	G/C N
330 331 332	G G	G G	G G	G	G G	G	ç G	G/C G	G T	G/C	c G	G/C N
333	T C	Č.	Ç	Č.	r C	C	T C	Ċ C	G A	N N	T C	N N
334 335	A A	A	A	A A	A A	A A	A A	A A	C T	N N	A A	N N
336 337	G A	G A	G A	G A	G A	G A	G A	G A	G A	G A	G A	G A
338 339	A G	A G	A G	A G	A G	A G	G A	R R	A C	R N	A G	R N
340 341	90	G	G C	G Ç	G G	G C	G A	G N Y A C	A C	N Z N N O O N N R N N N N N N N N N N N N N	G A	GIC 2 2 2 2 2 2 2 2 2 3 4 2 2 4 2 4 2 2 2 2
342 343	C A	C A	C A	C A	C A	C A	T A	Y A	A C	N N Y N	C A	N N
344 345	A	C A	C A	Č Č	C A	C A	Ç	C A/T	C	N	C T	Y N
348 347	c .	c c	c c	c c	Ç	c	G T	C/G	G	C/G N	c	C/G N
348 349 350	Ğ	A G	A G	A G	A G	A G	Ť G	A/T G	G A	N R	r c	N N
350 351	G C G T G G T C A A G A A G G C C C A C C A C C A G A G	T G C G T G G T C A A G A A G G C C A C A C C A G A G G A	G C G T G G T C A A G A A G G C C A C A C C A G A G G A	T G C G T G G T C A A G A A G G C C A C A C C A G A G G A	T G C G T G G T C A A G A A G G C C A C A C C A G A G G A	T G C G T G G T C A A G A A G G C C A C A C C A G A G G A	T G C G C C G T C A A G A G A G A T A C T G T T G A A G A	A/T C/G Y A/T G A R G A	G C A C G G T G A C T C A C A C A C T C C C G G A A G A T	C/G N N R A R R	T G T G C C G T C A A G A A G G A C A C T C C T C A G C A	C/G N N A R N AT
352 353	G A	G A	G A	G A	G A	G A	G A	G A	A T	R A/T	C A	N A/T
										1		

Fig. 7.2 cont.

Position 354 354 355 356 356 357 358 369 366 366 366 366 367 371 372 373 374 375 376 377 378 389 390 391 392 393 394 401 402 403 404 405 406 406	Tm1284-22 A C G G C T T A T G A C C T T C A G T T T T T T T T T T T T T T T T T T	Tm12 84-2-3 A A C C G G C T T A T G A C C C T T C A A G T G T A T T T A C G A C C T T G A T T T C T C T C C C	Tm12 84-3-4 A A C C G G C T T A T G A C C C T T C A A G G T T A T T T A C G A C C C T T C T C T C T C T C T C T C T	Tm12 84-39 A A C C G G C T T A T G A C C C T T C A A G T G T A T T T A C G A C C T T G A T T T C T C T C C C	Tm1284-75 A A C C G G C T T A T G A C C C T T C A A G T G T A T T T A C G A C C T T C C C T C T C C C T C T C C C T C C C T C C C T C C C T C C C T C C C T C C C T C C C T C C C T C C C C T C C C C T C C C C T C C C C T C C C C T C C C C C T C C C C C C C C C C C C C C C C C C C C	Concensus of A A C A C C T T A T G A C C C T T C A A G C C T T A T C C A A G C C C T T C A A C C C T T C C A A C C C T T C C C C	TM GACGGTGTTCAAATACTTTCAAAATGTGTCATGAAAAAACAAGCCA  AAGTTCTCACC	Concensus with RACCGGGYNTTTCAARNNTTRTYAATGRANARCCTIARNNTTRTYTAATGRANARCCCTIARNNTTCTCTCAACCTIARNARCCCTIARNNTTCTCTCCACCTIARNARCCCTIARNARCCCTIARNARCCCTIARNARCCCTIARNARCCCTIARNARCCCTIARNARCCCTIARNARCCCTIARNARCCCTIARNARCCCTIARNARCCCTIARNARCCCTIARNARCCCTIARNARCCCTIARNARCCCTIARNARCCCTIARNARCCCTIARNARCCCTIARNARCCCTIARNARCCCTIARNARCCCTIARNARCCCCTIARNARCCCCTIARNARCCCCTIARNARCCCCTIARNARCCCCTIARNARCCCCTIARNARCCCCTIARNARCCCCTIARNARCCCCTIARNARCCCCTIARNARCCCCTIARNARCCCCTIARNARCCCCTIARNARCCCCTIARNARCCCCTIARNARCCCCTIARNARCCCCTIARNARCCCCTIARNARCCCCCTIARNARCCCCTIARNARCCCCTIARNARCCCCTIARNARCCCCTIARNARCCCCTIARNARCCCCTIARNARCCCCTIARNARCCCCTIARNARCCCCTIARNARCCCCTIARNARCCCCTIARNARCCCCTIARNARCCCCTIARNARCCCCTIARNARCCCCTIARNARCCCCTIARNARCCCCTIARNARCCCCTIARNARCCCCTIARNARCCCCTIARNARCCCCTIARNARCCCCTIARNARCCCCTIARNARCCCCTIARNARCCCCTIARNARCCCCTIARNARCCCCTIARNARCCCCTIARNARCCCCTIARNARCCCCTIARNARCCCCTIARNARCCCCTIARNARCCCCTIARNARCCCCTIARNARCCCCTIARNARCCCCTIARNARCCCCTIARNARCCCCTIARNARCCCCTIARNARCCCCTIARNARCCCCTIARNARCCCCTIARNARCCCCTIARNARCCCCTIARNARCCCCTIARNARCCCCTIARNARCCCCTIARNARCCCCTIARNARCCCCTIARNARCCCCTIARNARCCCCTIARNARCCCCTIARNARCCCCTIARNARCCCCTIARNARCCCCTIARNARCCCCTIARNARCCCCTIARNARCCCCTIARNARCCCCTIARNARCCCCTIARNARCCCCTIARNARCCCCTIARNARCCCCTIARNARCCCCTIARNARCCCCTIARNARCCCCTIARNARCCCCTIARNARCCCCTIARNARCCCCTIARNARCCCCTIARNARCCCCTIARNARCCCCTIARNARCCCCTIARNARCCCCTIARNARCCCCTIARNARCCCCTIARNARCCCCTIARNARCCCCTIARNARCCCCTIARNARCCCCTIARNARCCCCTIARNARCCCCTIARNARCCCCTIARNARCCCCTIARNARCCCCTIARNARCCCCTIARNARCCCCTIARNARCCCCTIARNARCCCCTIARNARCCCCTIARNARCCCCTIARNARCCCCTIARNARCCCCTIARNARCCCCTIARNARCCCCTIARNARCCCCTIARNARCCCCTIARNARCCCCTIARNARCCCCTIARNARCCCCTIARNARCCCCTIARNARCCCCTIARNARCCCCTIARNARCCCCTIARNARCCCCTIARNARCCCCTIARNARCCCCTIARNARCCCCTIARNARCCCCTIARNARCCCCTIARNARCCCCTIARNARCCCCTIARNARCCCCTIARNARCCCTIARNARCCCCTIARNARCCCTIARNARCCCCTIARNARCCCTIARNARCCCTIARNARCCCTIARNARCCCTIARNARCCCTIARNARCCCTIARNARCCCTIARNARCCCTIARNARCCCTIARNARCCCTIARNARCCCTIARNARCCCTIARNARCCCTIARNARCCCTIARNARCCCTIARNARCCCTIARNARCCCTIARNARCCCTIARNARCCCTIARNARCCCTIARNARCCCTIARNARCCCTIAR	BACGCCATTTGAAGTTACCAAATGTGTATTGAAGGACAAGCCCA ATTTCTTTGC.	Concensus with R R R R R R R R R R R R R R R R R R R	AFP-3 CT C C T C A G C C G A C T T G T Y T A A A T G C G G T T C A C G A T A A C A G G T C G	Concensus with N N N N N N N N N N N N N N N N N N N
408 409 410 411 412 413 414 415 416 417 418 421 422 424 423 424 422 428 424 427 429 420 420 421 421 422 426 427 429 420 420 421 421 422 423 424 425 426 427 429 420 420 421 421 425 426 427 427 428 429 430 431 431 431 431 431 431 431 431 431 431	C T A T T G A T T G T T T T T G T A T T T T	C T A Y T G A T T T G T T T T T G A C T G A A T T T T G A C	C	C T A T T G A T T G T T T T T G T A T T T T	.C.T. A.T.T. G.T.T.T.T.T.T.T.T.T.T.T.T.T.T.T.T.	CTATTGAT. TAATTGTTTTTGTATTTGRCTGAATTTTGAC	CAGTTGAT•TGAACCACCACGACTAGTAGATGGTTCAAATGGTGTGCTTTACATATAAA	C C ART T T G A T • T R A IA Y C C IA Y Y IA C N A Y T IA G N N N R ARNT T Y R A N T G G T G T G C T T T A C A T A T A A A	A G A C T A T T T G T C T G A A A G C T T T G T G C A C A A	N N R Y T R ATT • T R ATN Y GUAN N N CONATY N MAGN N N R AR R N T T Y R A N T G G T G T G C T T T A C A T A T A A A	· TAATGGGGTCGCTCGAAGACTTATTATAATGTAAACCTTGCCAATTTTTTGAAC	· TRINNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN

Position	Tm12 84-2 2	Tm12 84-2 3	Tm12 84-3 4	Tm12 84-3 9	Tm12 84-7 5	Concensus of	Tm13 17	Concensus with	B1	Concensus with	AFP-3	Concensus with
472	A	Α	A	A	A	A	Α	Α		A	A	A
473	A	A	Α	Α	A	Α	Α	Α		Α	Α	Α
474	T	T	T	T	Ŧ	т	Ŧ	т		T	т	T
475	A	A	A	Α	A	Α	A	A		A	Α	Α
476	Α	A	Α	A	A	A	A	A		A	A	A
477	A	A	A	A	A	A	Α	A		A	A	Α
478	G	G	G	G	G	G	G	G		G	Т	N
479	G	G	G	G	G	G	T	N		N	T	N
480	T	T	T	T	T	T	G	N		N	т	N
481	Α	A	A	A	A	A	T	N		N	A	N
482	Α	¢	С	С	C	С	Т	Y		Y	A	N
483	Т	T	T	T	Т	T	T	т		٣	A	A/T
484	Α	A	A	A	A	Α	C	N		N	G	N
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Fig. 7.3

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Fig. 7.3 cont.

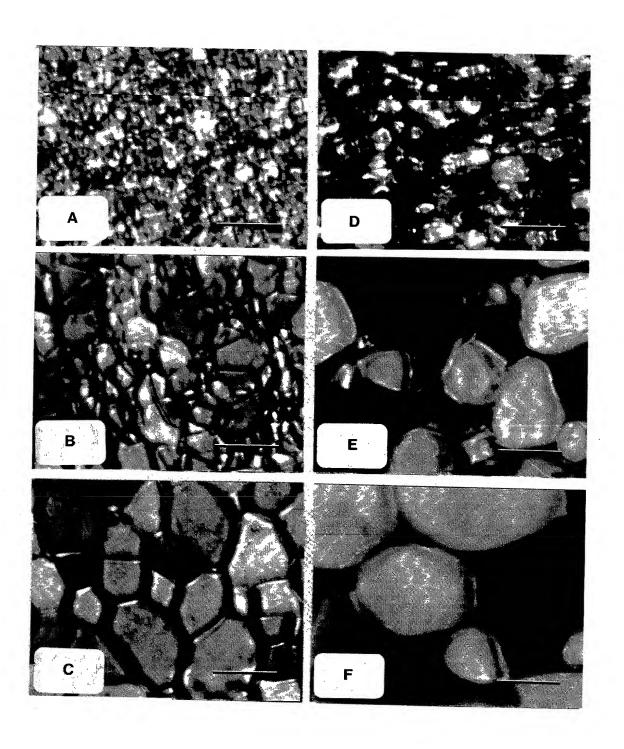


Fig. 8.0

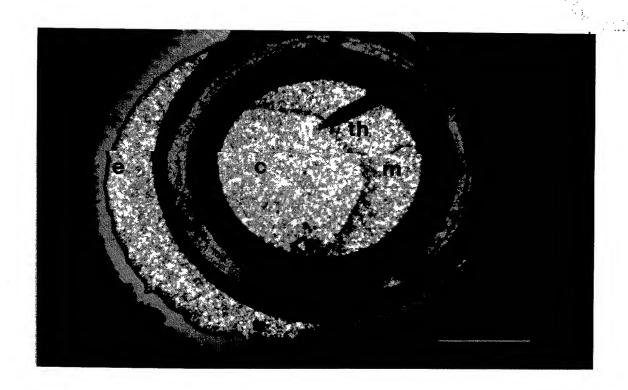


Fig. 8.1a

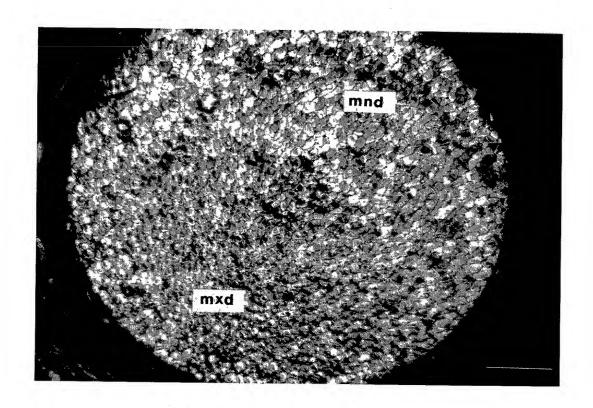
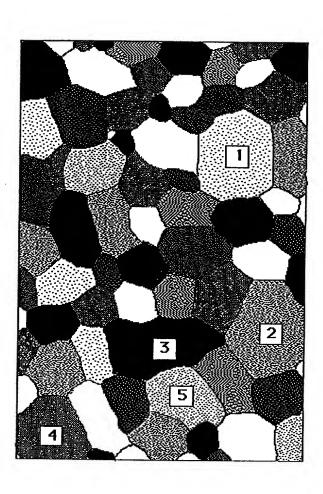
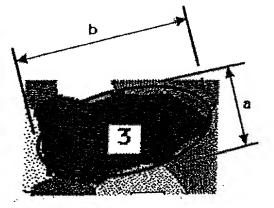
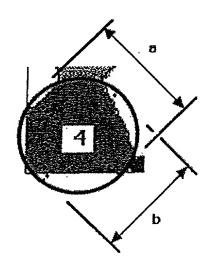


Fig. 8.1b





grain area=0.25mab



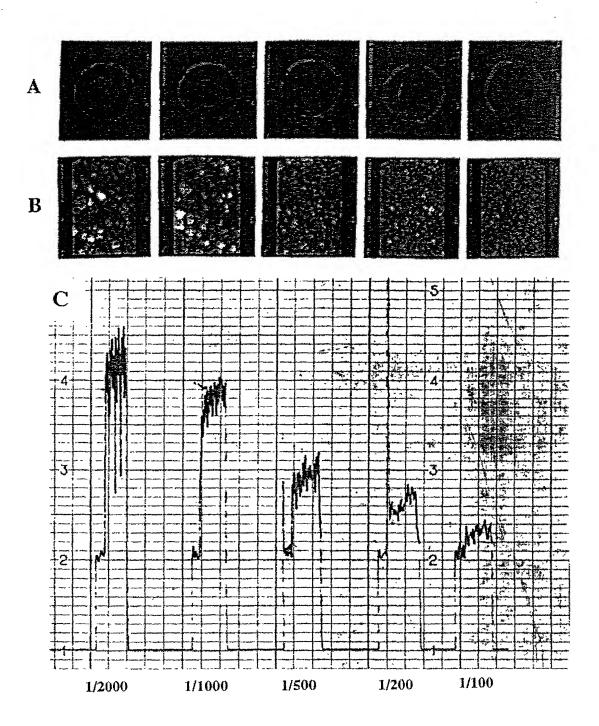
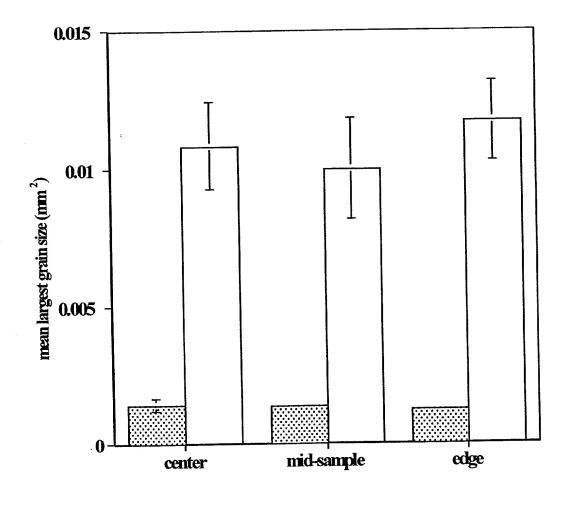


Fig. 8.3



category

Fig. 8.4a

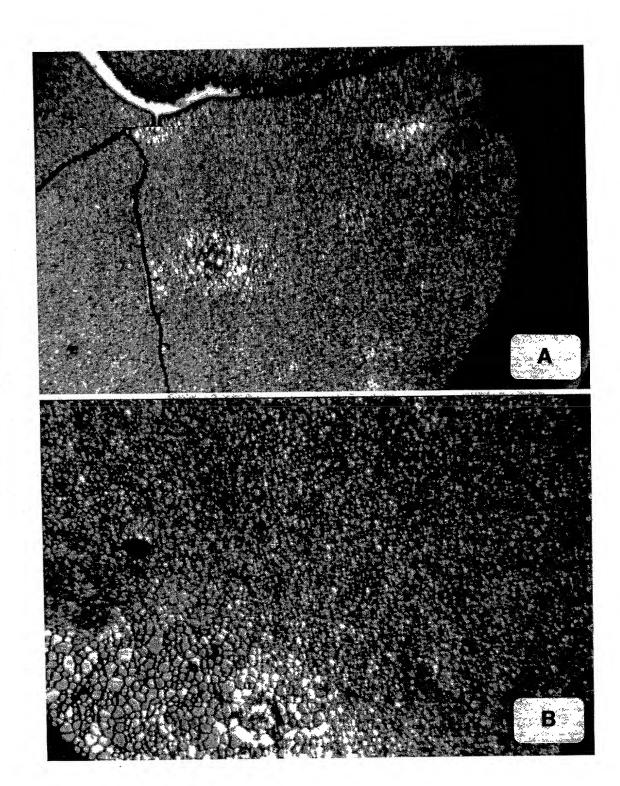


Fig. 8.4b

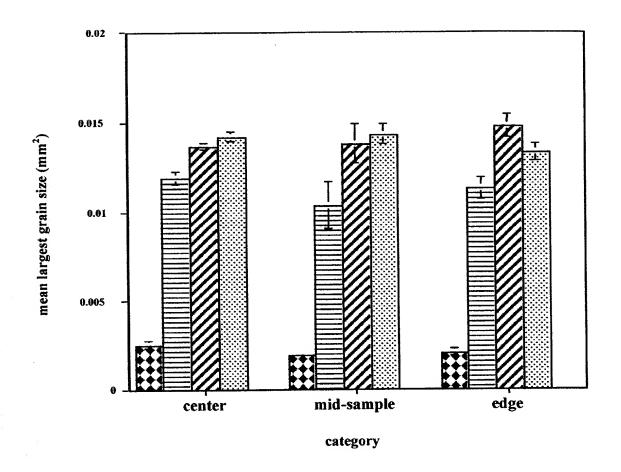


Fig. 8.5a

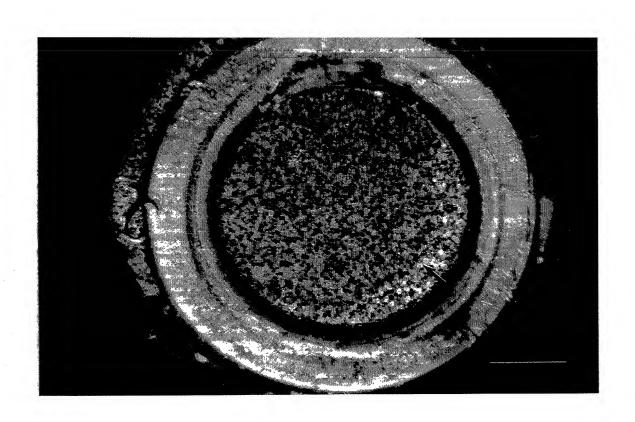


Fig. 8.5b

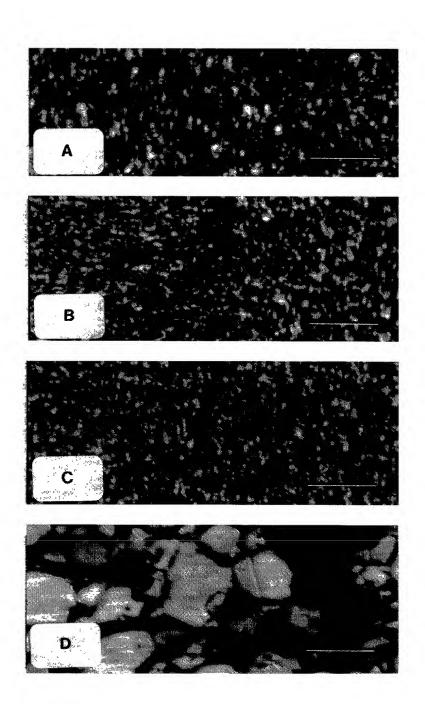


Fig. 8.6

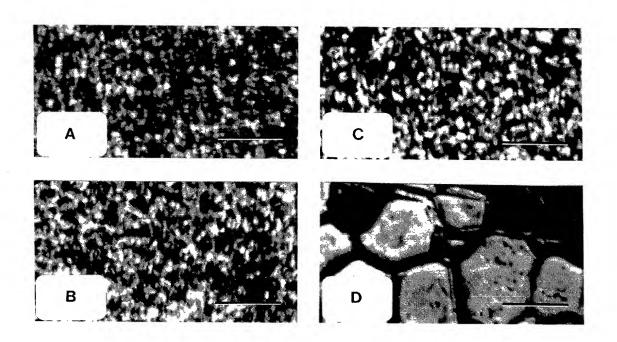


Fig. 8.7

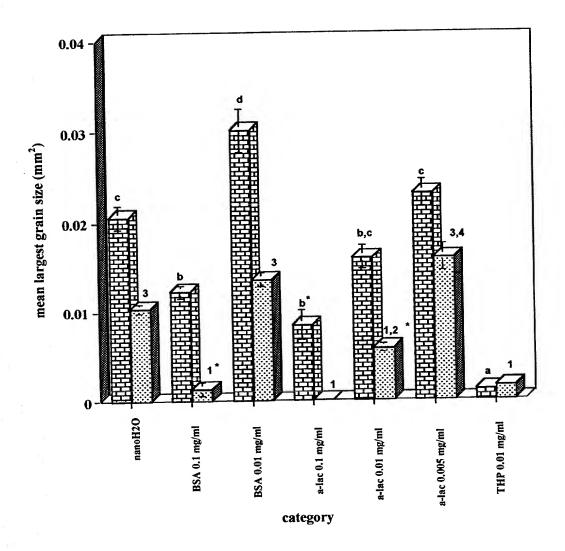


Fig. 8.8

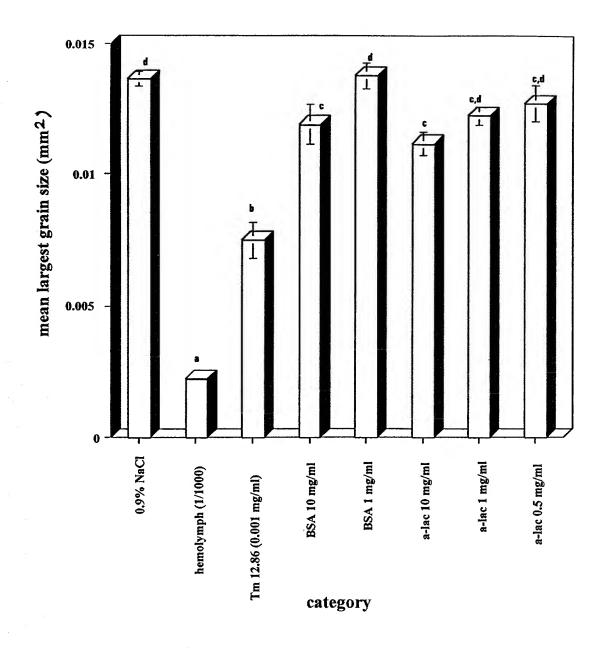
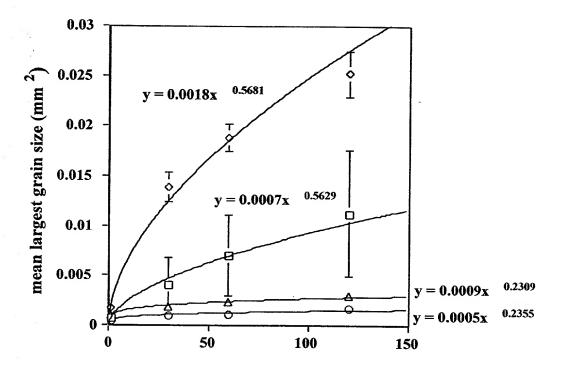


Fig. 8.9



time (minutes)

Fig. 8.10

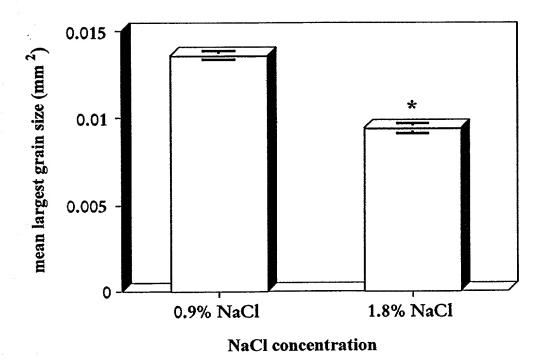


Fig. 8.11

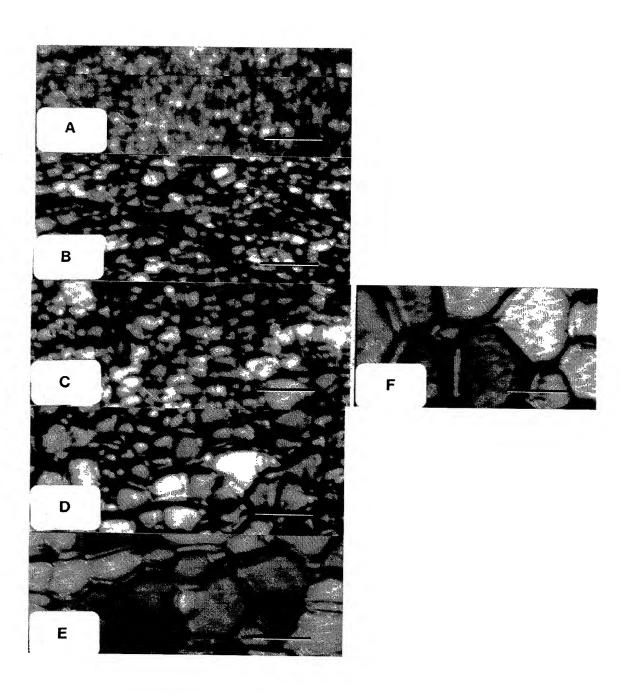
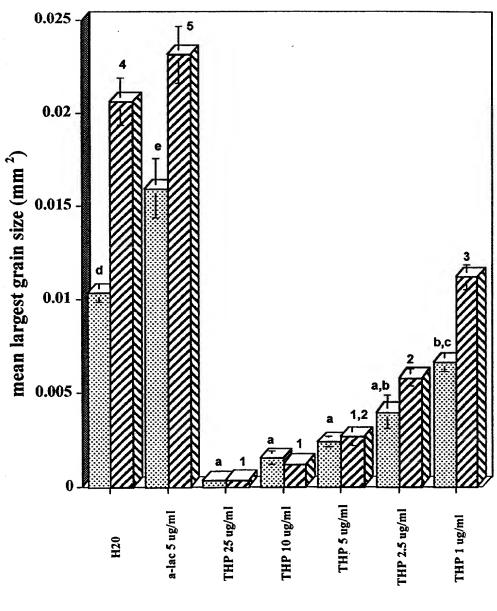


Fig. 8.12



composition

Fig. 8.13

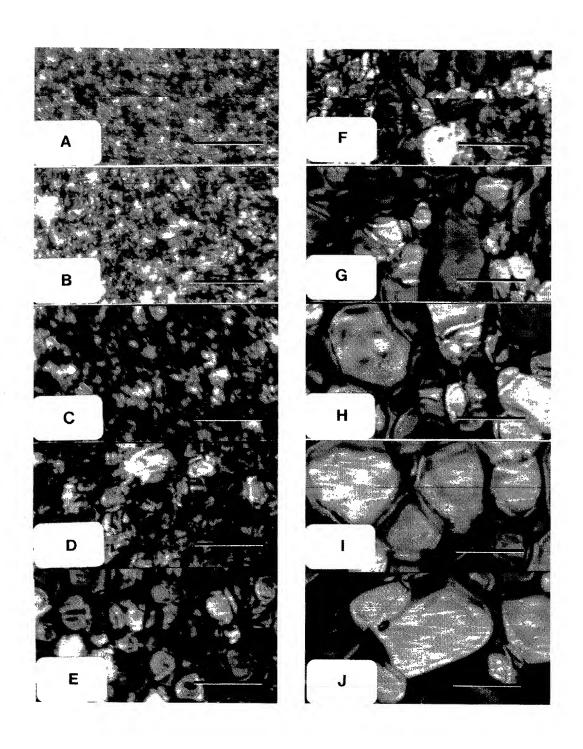


Fig. 8.14

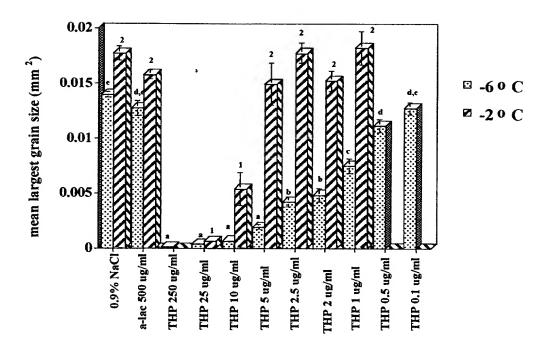
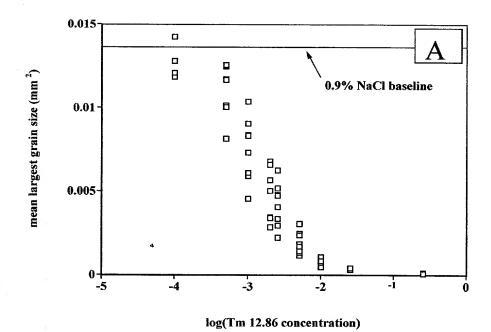


Fig. 8.15



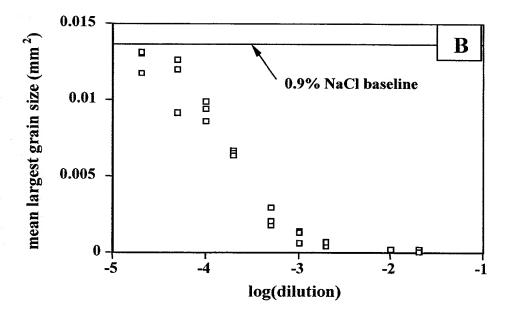
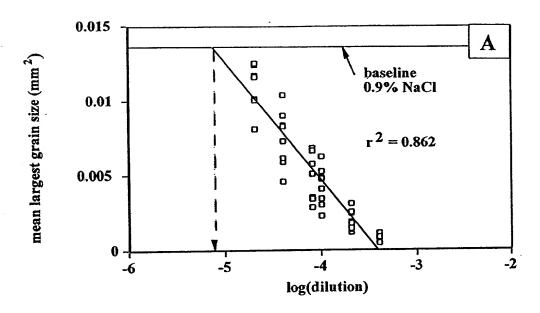


Fig. 8.16



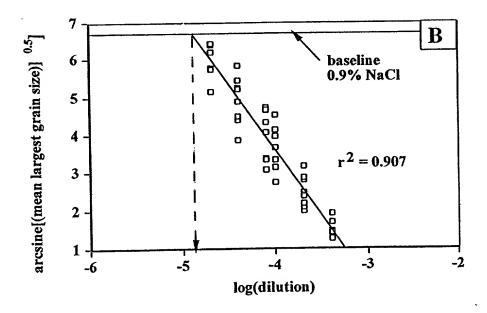
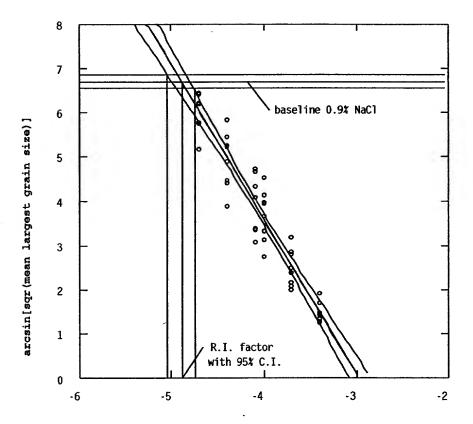
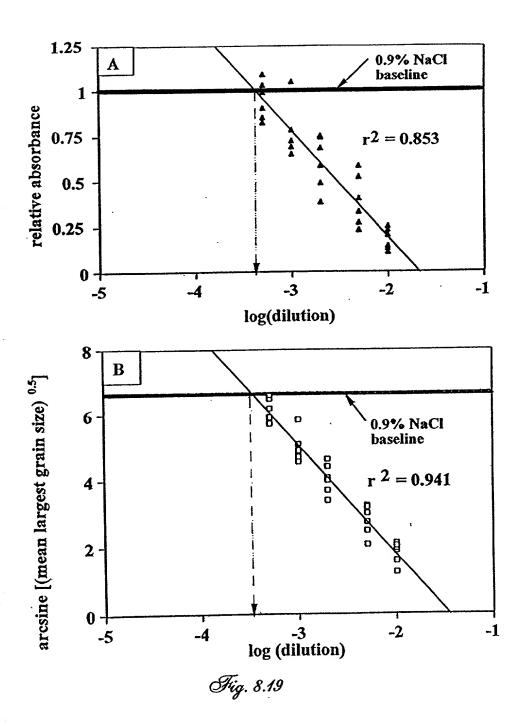


Fig. 8.17



log(dilution)

Fig. 8.18



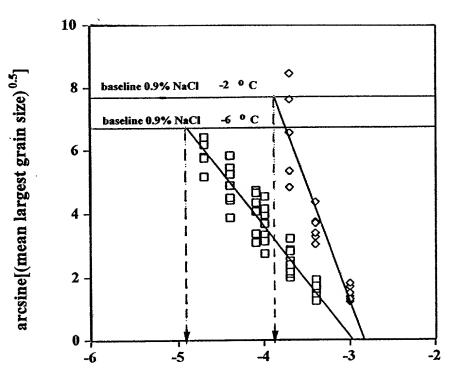
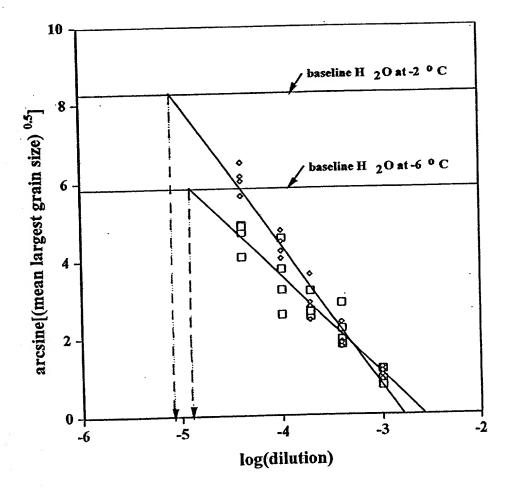
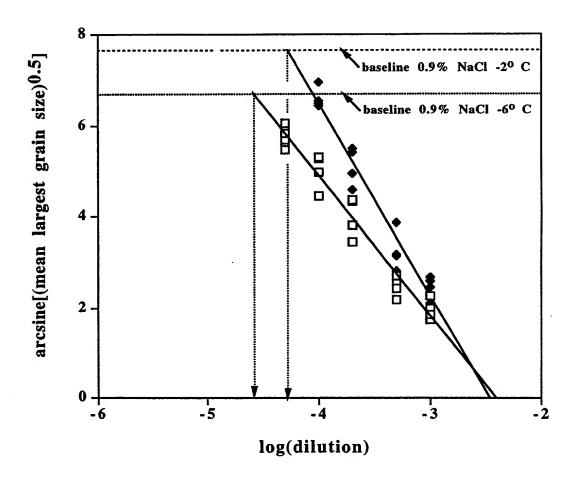


Fig. 8.20

log(dilution)





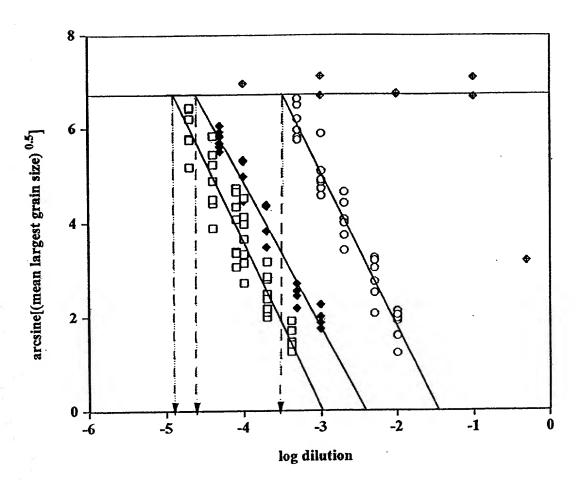
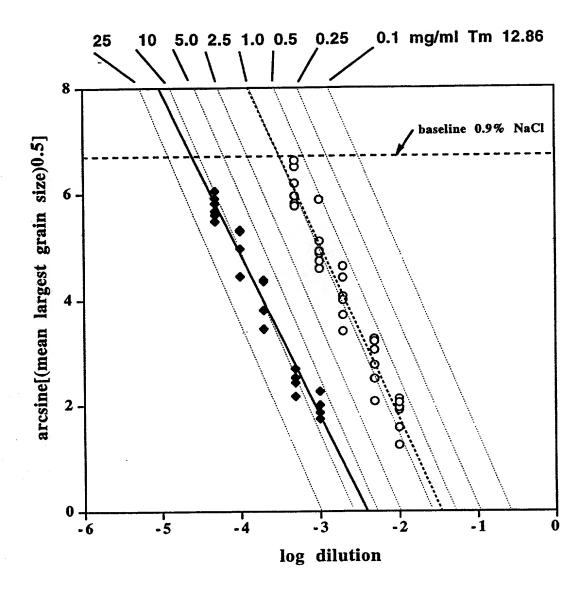


Fig. 8.23



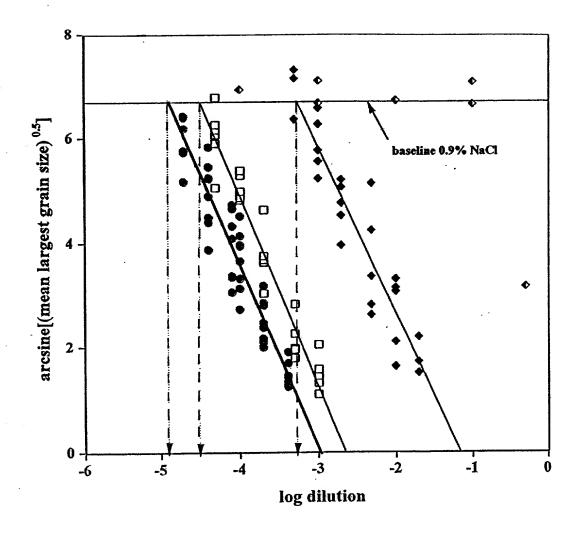


Fig. 8.25

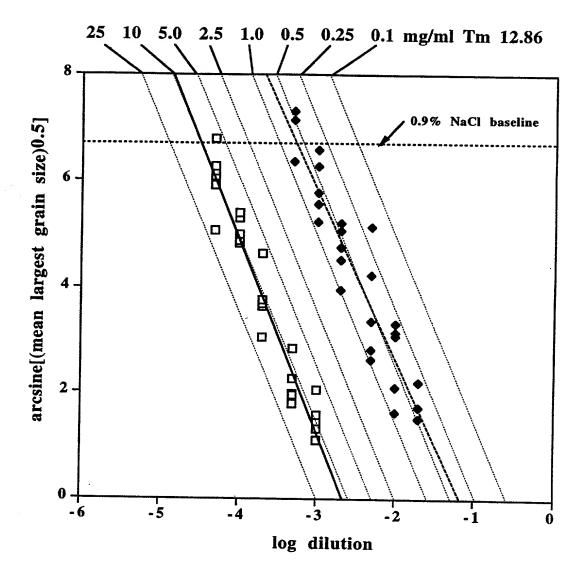


Fig. 8.26

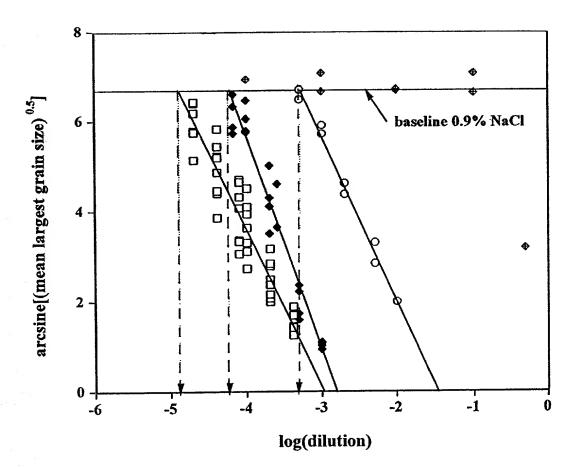


Fig. 8.27

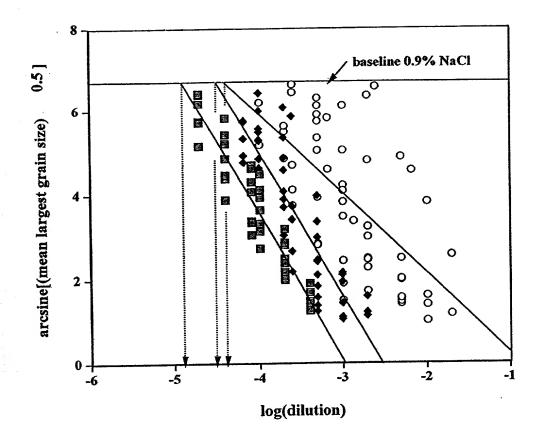
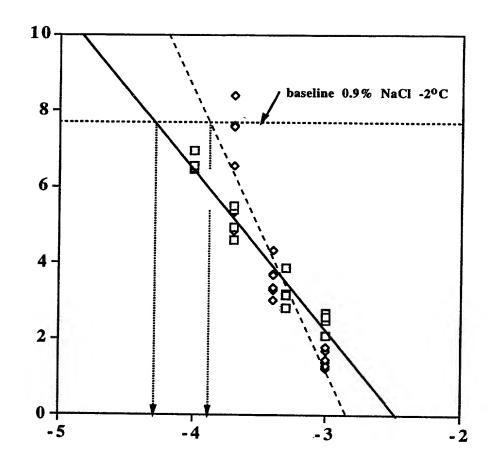


Fig. 8.28



log(dilution)

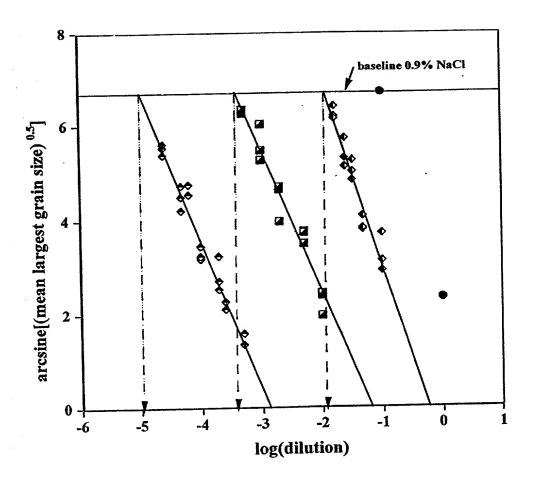


Fig. 8.30

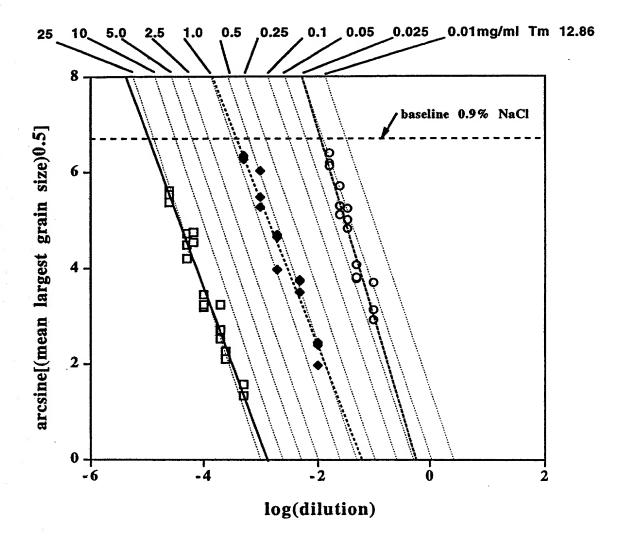
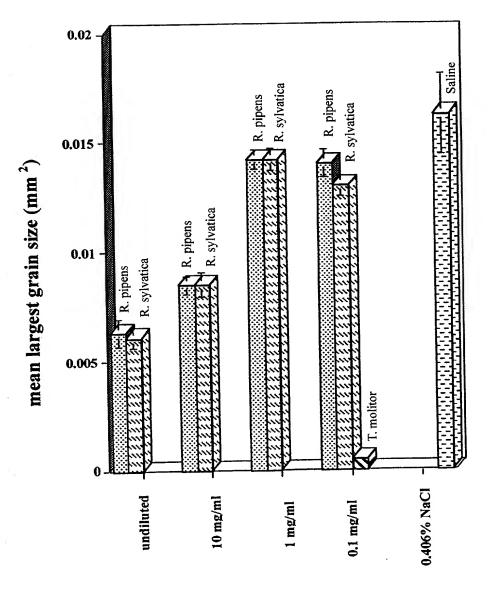


Fig. 8.31



dilution

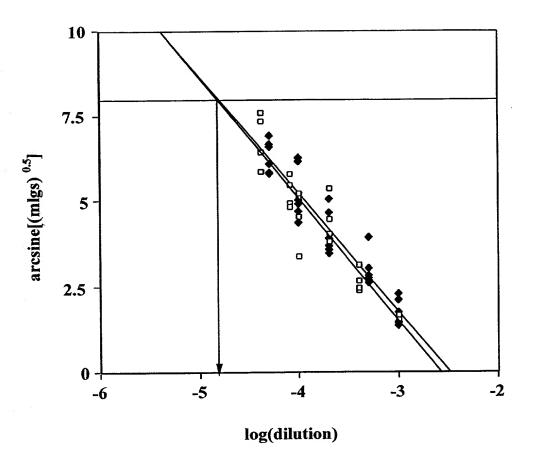


Fig. 8.33

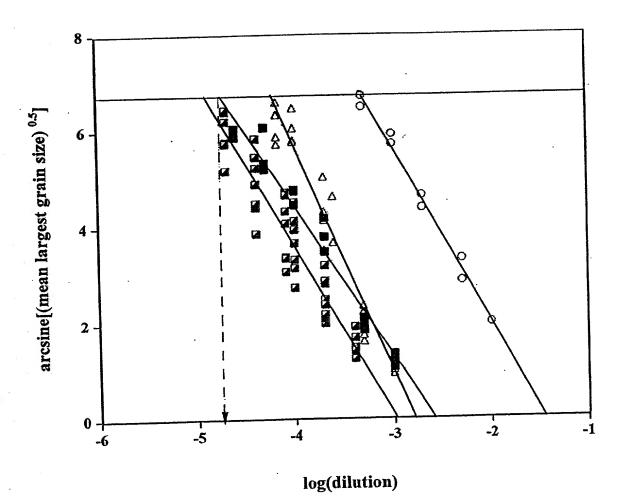
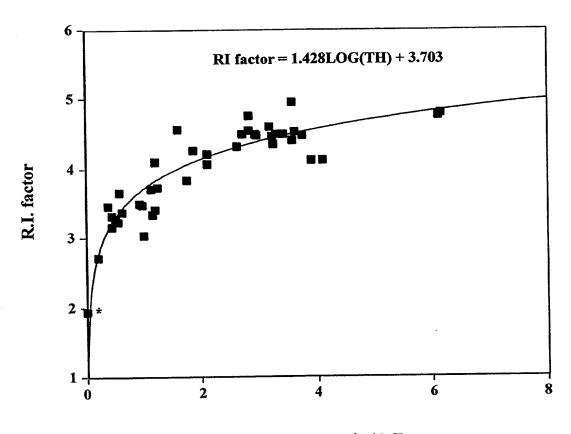
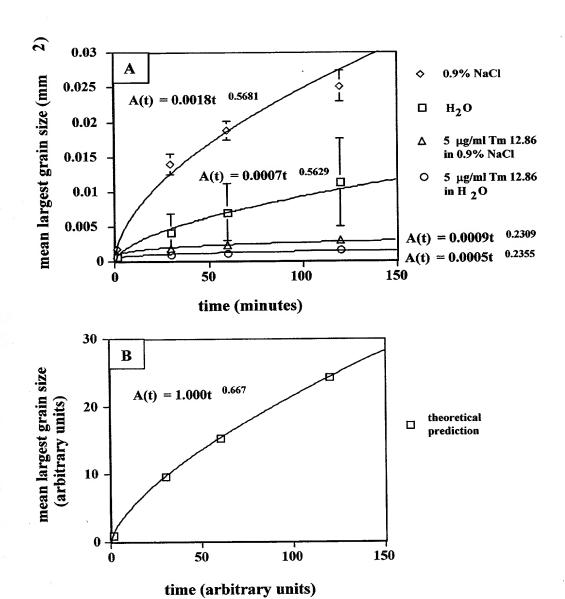
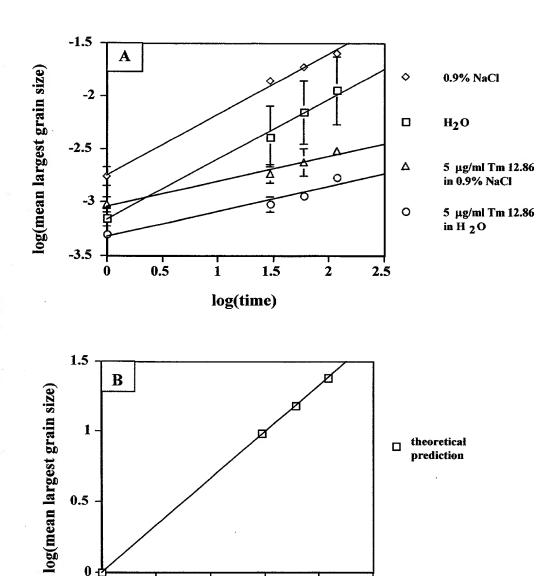


Fig. 8.34



thermal hysteresis (°C)





1.5

log(time)

1

2

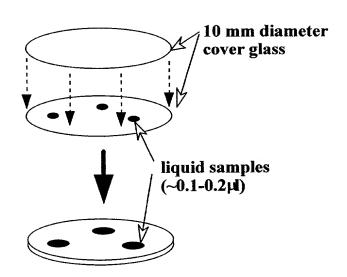
2.5

0.5

## "Sandwich" method of R.I. assessment

1.

2.





3. FREEZE ON ~-80 C ALUMINUM PLATE (~10 MIN.)



4. PLACE ON COLD STAGE, ANNEAL AT -6 C UP TO 12+ HOURS

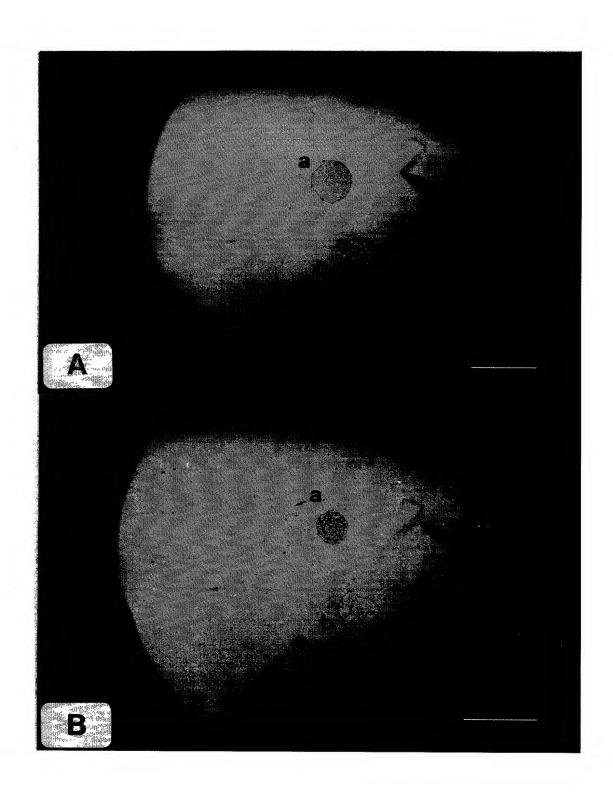


Fig. 8.39

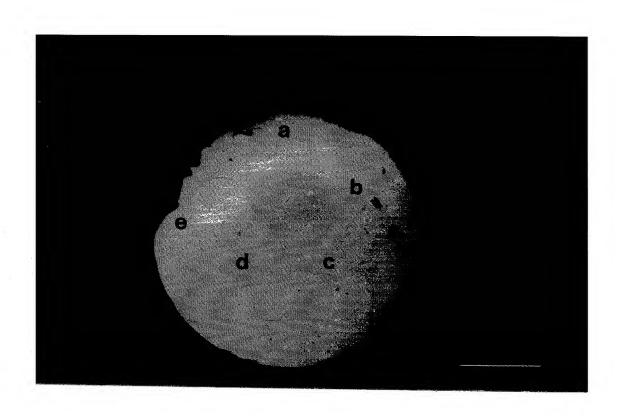


Fig. 8.40

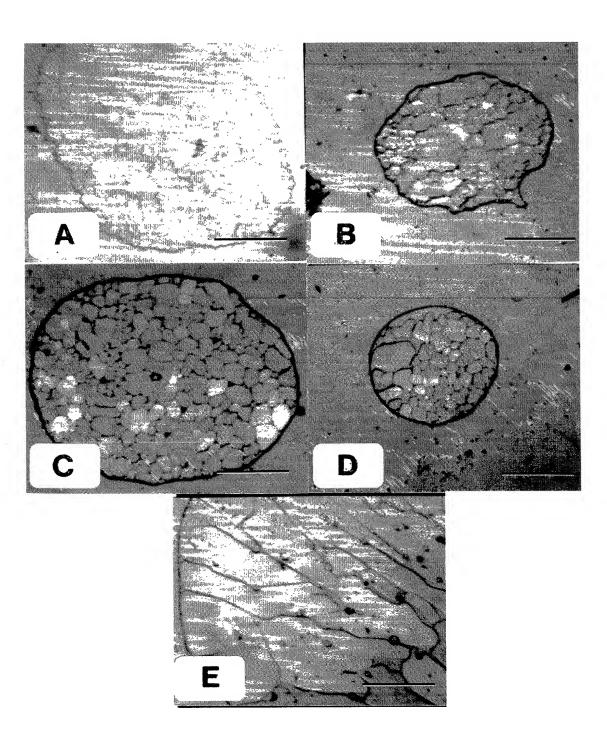
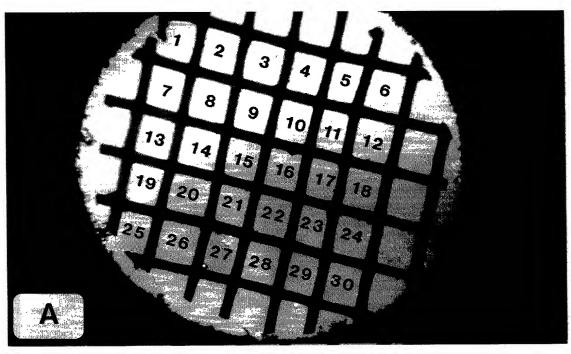


Fig. 8.41



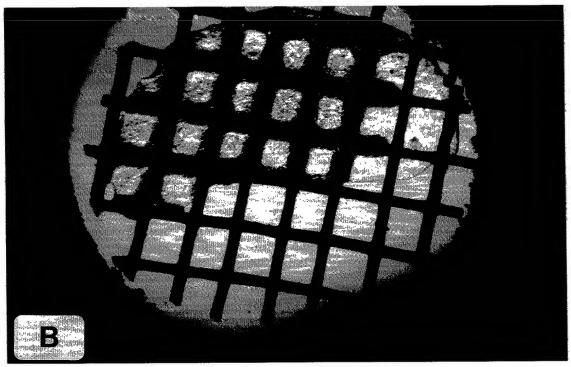


Fig. 8.42

## DNA sequence of Tm 13.17 cDNA clone

	В			E	k F															
	a			c	:															
	m	ı		C	•															
	H			R	ŧ.															
	I			Ί																
1	AGTG	Gat	CCA	AAG	raa:	TCG	GÇA	CGA	GAC	TAC	TAA	GAT	GAA	GT1	'GCT	CTG	TTG	TCT	TAA	CT
												M	K	I,	L	C	C	L	I	S
										_		G-				P				
61	CCCT	CAT	TCT	GTT	'GG'I	CAC	AGT	TCA	GGC	CO	GAC	CGA	GGC	ACA	AAT	TGA				
	L	I	L	L	V	T	V	Q	A	AL_	T	E	A	Q	I	E	K	Ļ	N	K
									,	T		Y								
121	AGAT	CAG	CAA	AAA	ATC	TCA	AAA	TGA	AAG	IGG	AGT	GTC	GCA	AGA	GAT	CAT	AAC	CAA	AGC	TC
	I	S	K	K	C	Q	N	E	S	G	V	S	Q	E	I	I	T	K	Ą	R
181	GCAA	CGG	TGA	CTC	:GGP	<b>IGGA</b>	CGA	TCC	AAT!	ACT	'GAA	ACG	CCA	AGT	TTI	TTG	CGT	GGC	CAG	GA
	N	G	D	W	E	D	D	P	K	L	K	R	Q	V	F	C	V	A	R	N
241	ACGC	CGG	TCT	'GGC	CAC	GGA	ATC	:GGG	AGA	GGT	'GGT	GGT	CGA	CGI	GTT	GAG	GGA	GAA	ggt	GA
	A	G	L	A	T	E	S	G	E	V	V	V	D	V	L	R	E	K	V	R
															P					
301	GGAA	GGT	CAC	TGA	CAP	CGA	CGA	AGA	AAC	TGA	GAA	TAA	CAT	CAA	TAA	GTG	CGC	CGT		GA
	K	V	T	D	N	D	E	E	T	E	K	I	I	N	K	C	A	V	K	R
	P			4																
361	GAGA	TAC	TGI	TGA	AGI	GAC	GGT:	GTT	CAA	TAC	TTT	CAA	ATG							
	D	T	A	E	E	T	V	F	N	T	F	K	C	٧	M	K	N	K	P	K
				G																
421	AGTT	CTC	ACC	AGT	TG	TTC	AAC	CAC	CAC	GAC	TAG	TAG	ATC	GTI	CAA	ATG	GTG	TGC	TTT	AC
	F	S	P	V	D	*														
																			X	•
																			h	ì
																			.C	<b>&gt;</b>
																			1	
481	ATAT	AAA	AA:	TAA	AG	rGT1	TCI	GAT	GTA	AA	AAA	AA	AAA	AA	AA	AAI	LAA	AAA	AA.	CTCC

polyadenylation signal poly (A) tail (26)

537 AGAGTATTCTAGAGCGGCCGCGGGCCCATCGTTTTCCACCC

GGCACGAGCAAAA<mark>ATG</mark>AAACTCCTCTTGTGCTTTG<u>CGTTCGCCGCC</u> M K L L C F A F A A ATCGTCATCGGAGCAGCAGACAGAAAA VIGAQALTDEQIQK 47 AGGAACAAGATCAGCAAAGAATGCCAGCAGGTGTCCGGAGTGTCCR N K I S K E C Q Q V S G V S 92 CAAGAGACGATCGACAAGTCCGCACAGGTGTCTTGGTCGATGAT Q E T I D K V R T G V L V D D CCCAAAATGAAGAAGCACGTCCTCTGCTTCTCGAAGAAAACTGGA P K M K K H V L C F S K K T G 182 GTGGCAACCGAAGCCGGAGACACCAATGTGGAGGTACTCAAAGCCVA TEA G D T N V E V L K A 226 AAGCTGAAGCATGTGGCCAGCGACGAAGAGGTGGACAAGATCGTG K L K H V A S D E E V D K I V CAGAAGTGCGTGGTCAAGAAGGCCACAGAGGAAACGGCTTAT Q K C V V K K A T P E E T A Y 316 361 ATTGATTAATTGTATTTGACTGAATTTTGACAAAAGGT 406 polyadenylation signal ACTATOGTTATGTAAAAAAAAAAAAAAAAAA 451

poly (A) tail